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The Human Leukocyte Platelet-activating Factor Receptor

cDNA CLONING, CELL SURFACE EXPRESSION, AND CONSTRUCTION OF A NOVEL EPITOPE-BEARING ANALOG*

(Received for publication, June 12, 1991, and in revised form, October 14, 1991)

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A human myeloid transcript of approximately 4 kilobases was cloned as a cDNA from an expression library based on homology with the guinea pig cDNA recently described by Honda *et al.* (Honda, Z.-I., Nakamura, M., Miki, I., Minami, M., Watanabe, T., Seyama, Y., Okado, H., Tok, H., Ito, K., Miyamoto, T., and Shimizu, T. (1991) *Nature* 349, 342-346) as a receptor for platelet-activating factor (PAF). The cloned DNA confers high affinity binding sites for platelet-activating factor when transfected into COS-7 cells and has binding and desensitization properties similar to the human leukocyte receptor. Southern analysis using this cDNA indicates that the PAF receptor gene is present as a single copy in the human genome. The deduced protein sequence predicts seven hydrophobic regions for the PAF receptor, characteristic of the rhodopsin gene family, and is 83% identical to the deduced protein sequence of the corresponding guinea pig molecule. A modified human PAF receptor cDNA was constructed by inserting an additional 30 nucleotides after the 5'-ATG, encoding the amino acid sequence MDYKDDDDKEF, which is specifically recognized by a monoclonal antibody. The modified cDNA encodes a functional PAF receptor and is detected by antibody on the membrane of transfected COS-7 cells. The use of this construct supports the structural model for the rhodopsin-like superfamily of receptors which places the NH₂-terminal sequence on the extracellular side of the membrane, and should additionally be useful for affinity purification of the receptor protein.

The phospholipid, platelet-activating factor (PAF),¹ displays a wide variety of biological functions *in vivo*, including

* This work was supported by National Institutes of Health Grant HL 36162. While this manuscript was in review, Nakamura *et al.* (34) and Ye *et al.* (35) also reported cDNA sequences for the human PAF receptor. The sequences reported are identical to the one reported herein, with the exception of a T → C substitution at nucleotide 471 which makes no change in the amino acid. The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked "advertisement" in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

The nucleotide sequence(s) reported in this paper has been submitted to the GenBank™/EMBL Data Bank with accession number(s) M76674.

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¹ The abbreviations used are: PAF, platelet-activating factor; kb, kilobase; PCR, polymerase chain reaction.

granulocyte activation and chemotaxis, platelet activation, enhancement of vascular permeability, smooth muscle contraction, bronchospasm, and hypotension (1-4). These anaphylactoid actions occur in response to nanomolar quantities of PAF, and are mediated by specific receptors which are pharmacologically coupled to GTP-binding proteins (5-7). Pharmacologic studies with antagonist compounds and binding parameters suggest that there may be multiple receptors for PAF (8, 9).

Platelet-activating factor is known to be made up of a complex group of structurally related phospholipids characterized by an ether linkage at the *sn*-1 position, an acetyl moiety at *sn*-2 and a choline head group at *sn*-3 (10-12). Variations in the alkyl chain length have been observed or synthesized at both the 1 and 2 positions, and there are stereospecific requirements for biological function as well. No pharmacologic subclassification of PAF receptors has arisen from structure-activity studies with PAF analogs.

Recently Honda *et al.* (13), reported the molecular cloning of a guinea pig lung receptor for PAF identified by expression in *Xenopus* oocytes. Because of questions arising in the human system relating to the number and identity of PAF receptor(s), we screened a U937 myeloid cell expression library using a probe prepared from guinea pig lung cDNA. In this article, we report the cloning and expression of a high affinity human receptor for PAF, and present immunohistochemical data on the topology of the receptor in transfected cell membranes.

EXPERIMENTAL PROCEDURES

Materials—Reagents and enzymes used in the construction of cDNA were products of Boehringer Mannheim. pCDM8 vector and *Escherichia coli* MC1061/p3 were the gift of Dr. Brian Seed, Harvard Medical School. PCR reagents and the thermal cycler were products of Perkin-Elmer Cetus. WEB2086 was provided by Boehringer Ingelheim. COS-7 cells were obtained from the American Type Culture Association. [³H]Hexadecyl-PAF (60 Ci/mmol) was obtained from Du Pont-New England Nuclear. Northern and Southern hybridizations were performed with GeneScreen Plus membranes using protocols recommended by Du Pont-New England Nuclear. Anti-Flag M5 antibody was a generous gift from Immunex. Peroxidase-labeled anti-mouse IgG was a product of Vector Laboratories.

Molecular Cloning of a Myeloid PAF Receptor—Oligonucleotides corresponding to the 5'- and 3'-coding sequences for the guinea pig PAF receptor were prepared containing *Bam*HI sites (5'-CCGGATCCGAGCCATGGAGTTAAACAGA-3', sense; 5'-CCGGATCCAGCAGCAGAACTAATT-3', antisense). Guinea pig lung total RNA (2 µg) (14) was reverse transcribed with 20 units of avian myeloblastosis virus reverse transcriptase and 1 µg of oligo(dT) primer (15). This mixture was next added to a PCR reaction mixture containing 1 µM each of the sense and antisense primers described above, according to the recommendations provided with AmpliTaq DNA polymerase. Five cycles of PCR were performed with oligonucleotide hybridization at 45 °C, and 30 subsequent cycles performed at 65 °C. The band at approximately 1 kb was isolated following agarose gel electrophoresis

of a portion of the reaction mixture (GeneClean, Bio101, La Jolla, CA), and was labeled using random primers and [32 P]dCTP. This probe was used to screen a U937 cDNA library constructed in the expression vector pCDM8 as previously described (16). The colonies were hybridized under conditions of low stringency using 25% formamide, $5 \times$ SSC, $1 \times$ Denhardt's solution, and 0.1% sodium pyrophosphate at 37°C for 18 h. Filters were washed in $2 \times$ SSC at room temperature for 30 min with three exchanges and autoradiographs exposed for 24 h at -70°C using an image intensifying screen. Positively hybridizing colonies in the primary library were purified and characterized. A clone, CS1, was identified by sequence analysis to contain a full length coding sequence with significant similarities to the guinea pig lung PAF receptor cDNA. This clone was extensively sequenced on both strands using the dideoxy technique with double stranded template (17). Several partial length clones were also characterized from an HL60 cell library (generous gift of Dr. Stuart Orkin, Harvard Medical School), and these sequences all yielded an unambiguous structure.

Genomic DNA and RNA Analyses—Genomic DNA was prepared from peripheral blood leukocytes (18) and 7.5- μg aliquots were digested with restriction enzymes in 20- μl aliquots overnight at 37°C . Samples were electrophoresed at 5 V/cm through 0.9% agarose gels in $1 \times$ TAE (Tris acetate/EDTA) buffer and blotted to GeneScreen Plus membranes by capillary action according to the manufacturer's instructions. Hybridization was performed in 50% formamide at 42°C overnight using 10^6 cpm/ml of [32 P]dCTP-labeled insert of clone CS1. Final washing conditions were $0.2 \times$ SSC and room temperature for 30 min. Autoradiographs were prepared using an image intensifying screen for 24 h at -70°C . Polyadenylated RNA was prepared with oligo(dT)-cellulose (Collaborative Research, Bedford, MA) (19) using RNA from undifferentiated U937 cells, from U937 cells differentiated for 72 h with 1 mM dibutyryl-cAMP, or from bronchiectatic human lung parenchyma resected from a patient with cystic fibrosis. Samples of 2 μg were denatured using formaldehyde and electrophoresed through 0.9% agarose. Transfer to GeneScreen Plus membranes, hybridization, and washing were accomplished as described above. Autoradiographs were prepared using an image intensifying screen at -70°C for 7 days.

Construction of Flag-PAF Receptor cDNA—The Flag/pCDM8 construct was created to allow COS cell expression of Flag fusion proteins (20). A synthetic duplex oligonucleotide, 5'-AGCTTCCA GCA GCC ATG GAC TAC AAG GAC GAC GAT GAC AAA GAATTC-3', bearing a HindIII site and an EcoRI site, was ligated to a modified pCDM8 vector containing a pBluescript polylinker. The oligonucleotide bears the consensus sequence corresponding to the human NK-2 receptor (21) 5' to the ATG at position 15, which subsequently encodes the Flag sequence, MDYKDDDDKEF. An insert encoding the human PAF receptor was prepared by PCR using a primer which mutated the normal initiating methionine to a leucine (ATG \rightarrow CTG), placing the PAF receptor sequence downstream from the initiating methionine ATG for the Flag sequence.

COS Cell Expression of the Human Myeloid PAF Receptor—COS-7 cells were plated at a density of 10^6 cells/10-cm dish following trypsinization, and were grown for 18–24 h in Dulbecco's modified Eagle's medium supplemented with nonessential amino acids, sodium pyruvate, 6 mM glutamine, and 10% fetal calf serum. Cells were transfected with 2 μg of plasmid in 3 ml of Dulbecco's modified Eagle's medium containing 10% NuSerum (Collaborative Research), 1 mM chloroquine (freshly prepared, Sigma), and 400 $\mu\text{g}/\text{ml}$ of DEAE-dextran (Sigma). Transfections were incubated at 37°C in an atmosphere of 5% CO_2 in air for 2.5–3 h. The cells were then shocked with 10% dimethyl sulfoxide in phosphate-buffered saline for 5–10 min at room temperature and returned to media containing 10% fetal calf serum. 72–90 h following transfection the cells were washed with binding buffer consisting of 0.15 M choline chloride, 10 mM Tris-HCl, pH 7.5, 10 mM MgCl_2 , and 0.25% bovine serum albumin, and incubated in the same buffer with 2 nM ^3H -labeled PAF and appropriate concentrations of unlabeled PAF or WEB2086 for 30 min at 4 or 22°C . Uptake of radiolabeled ligand as a function of time was determined at 4°C . Desensitization of binding was performed by preincubating transfected cells with increasing concentrations of unlabeled PAF for 20 min at 4°C , washing, and subsequently incubating with 2 nM ^3H -labeled PAF for 30 min at 4°C . Cells were washed with binding buffer, solubilized with 0.5% Triton X-100, scraped into scintillation vials, and cell-associated ligand determined by scintillation counting. Nonspecific binding was determined in the presence of 10 μM unlabeled PAF. The K_d was determined from Scatchard analysis of the data obtained from duplicate points and

three separate transfection experiments.

Immunohistochemical Staining of Flag-PAF Receptor in COS-7 Cells—COS-7 cells transfected with the Flag-PAF receptor/pCDM8 plasmid described above were incubated for 20 min at 22°C with 0 or 3 μM PAF in binding buffer. They were subsequently incubated with 10 $\mu\text{g}/\text{ml}$ of anti-Flag M5 monoclonal antibody in Tris-buffered saline containing 1 mM CaCl_2 (TBS/Ca), 3% bovine serum albumin, 0.5% normal horse serum, and 0.1% sodium azide for 1 h at 4°C . Cells were washed $3 \times$ with TBS/Ca, fixed with 2% paraformaldehyde in phosphate-buffered saline for 15 min at 4°C , and incubated with biotinylated horse anti-mouse IgG followed by peroxidase-labeled avidin-biotin complex as recommended by the manufacturers. Cells were stained with 0.05% diaminobenzidine and 0.01% H_2O_2 in TBS/Ca, counterstained with methylene blue, coverslipped with Permount, and photographed.

RESULTS

The guinea pig lung PAF receptor cDNA (13) was prepared by PCR and used to identify an analogous human clone by hybridization with a U937 cell expression library. The longest clone obtained, pCS1, contains a cDNA of approximately 2.8 kb which hybridizes to a single transcript in U937 cell RNA of approximately 4 kb (Fig. 1, lane A). Differentiation of the cells with 1 mM dibutyryl-cAMP for 72 h leads to an apparent decrease in abundance of this message (lane B). The same ~4-kb transcript is observed in human lung, as shown in lane C.

Analysis of genomic DNA with pCS1 under conditions of high stringency reveals a single restriction fragment hybridizing with the probe. As depicted in Fig. 2, digests using *Bam*HI, *Eco*RV, *Hind*III, or *Pst*I yield prominent hybridization signals. Analysis of murine genomic DNA digested with the same restriction enzymes, and hybridized and washed under conditions of high stringency reveals a similar pattern, although the fragments are not always the same size (data not shown). These data suggest that pCS1 encodes a single copy gene common to mouse and man. Prolonged exposure of Southern blots reveals a faint background of cross-hybridizing bands, which may reflect related genes (data not shown).

The cDNA and deduced protein sequences of clone CS1 are presented in Fig. 3. The longest open reading frame encodes a protein of 342 amino acids, and search of the EMBL and GenBank data base releases through 1990 revealed no closely related structures. Examination of the deduced protein sequence reveals seven hydrophobic regions interspersed with polar peptide segments characteristic of rhodopsin type G protein-dependent receptors. In contrast to all other identified members of the rhodopsin family of receptors reported to date, including the PAF receptor from guinea pig, the amino-terminal domain of the human PAF receptor does not contain an N-linked glycosylation site. An Asn-X-Thr/Ser sequence is observed at positions 169–171, and a second potential N-linked glycosylation site is found at positions 333–335 at the COOH terminus.

Clone pCS1 in the expression vector pCDM8 was trans-

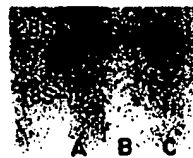
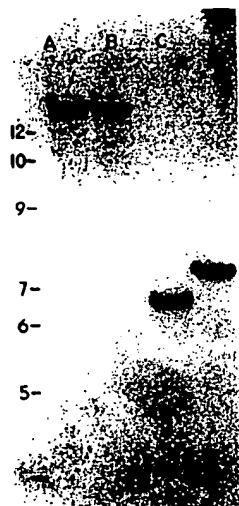


FIG. 1. Northern analyses of myeloid cell and lung RNA. Two μg of polyadenylated RNA was analyzed under denaturing conditions as described under "Experimental Procedures." Lane A, undifferentiated U937 cells; lane B, U937 cells differentiated for 72 h with 1 mM dibutyryl-cAMP; lane C, human lung parenchyma. A single transcript of ~4 kb was observed to hybridize with cDNA clone pCS1 under conditions of high stringency.



We constructed a Flag-PAF receptor cDNA plasmid, in which the initiating methionine of the natural PAF receptor is mutated to a leucine by PCR and ligated to pCDM8 containing a 5' adapter encoding the Flag sequence, MDYK-DDDDKEF. The Flag sequence, including the NH₂-terminal methionine residue, is specifically recognized by a monoclonal

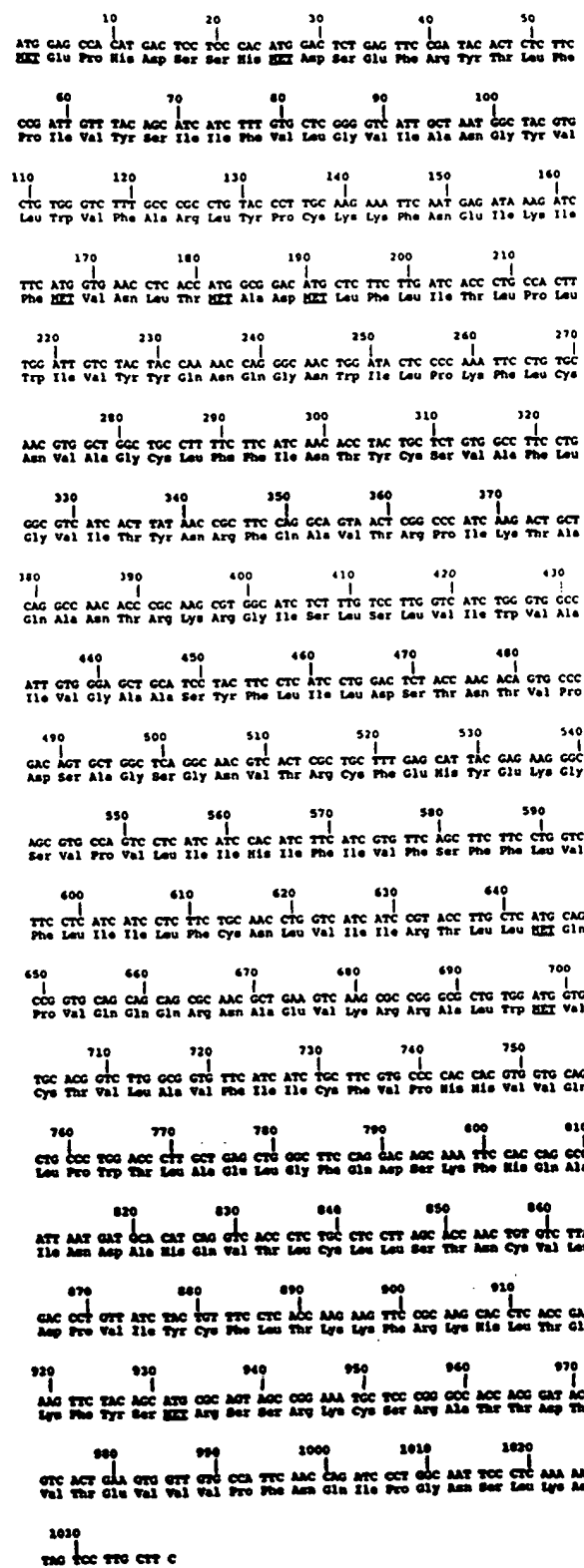


FIG. 3. cDNA and deduced protein sequence for the human PAF receptor. Clone pCS1 was sequenced extensively on both strands, and clones from the U937 and HL60 cDNA libraries were identical. The complete coding sequence is depicted, and the deduced protein structure contains 342 amino acids. Primers encompassing the first and last 18 nucleotides depicted are useful in PCR, yielding full length human PAF receptor cDNA.

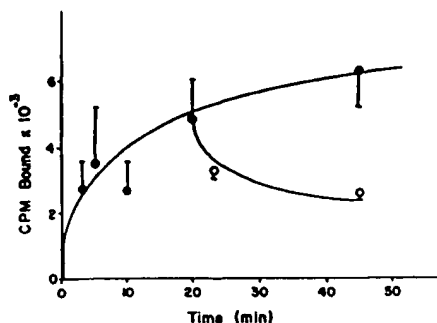


FIG. 4. Kinetics of binding of ^3H -labeled PAF to transfected COS-7 cells. COS-7 cells 72 h after transfection with clone pCS1 were incubated with 2 nM ^3H -labeled PAF at 4 °C as detailed under "Experimental Procedures." Each point represents the mean of duplicate determinations. Nonspecific binding was assessed by binding in the presence of 10 μM PAF.

antibody, M5, in the presence of millimolar concentrations of calcium (20). Transfection of the Flag-PAF receptor/pCDM8 construct into COS-7 cells also confers specific PAF receptor activity (Fig. 5A). Scatchard analysis suggests a slightly lower binding affinity for the ligand, but a similar number of sites per cell (Table I). Thus expression of the Flag-PAF receptor molecule is comparable to the unmodified receptor when transfected into COS cells, and is presumably oriented in a similar manner on the cell membrane. In order to confirm the model for this receptor protein, as illustrated in Fig. 7 which is based on the structure of rhodopsin, transfected cells were stained with the M5 monoclonal antibody followed by secondary antibody and horseradish peroxidase-labeled avidin-biotin complex. As indicated in Fig. 8, the epitope appears to be localized on the extracellular side of the membrane. Nontransfected cells show no staining with this antibody.

DISCUSSION

The U937 cell line is a human lymphoma clone with myeloid characteristics (23), and contains receptors for many proinflammatory mediators including C5a anaphylatoxin, the bacterial chemotaxin, formyl-Met-Leu-Phe, leukotrienes B_4 and D_4 , and interleukin-8, as well as PAF (16). Expression of many of these receptors may be modulated positively or negatively by driving differentiation of the cells towards macrophage-like cells with phorbol esters, or towards cells with the phenotype of monocytes and neutrophils with dibutyryl-cAMP (24). The human PAF receptor cDNA was cloned from an undifferentiated U937 cell library by hybridization with the cDNA corresponding to the guinea pig PAF receptor (13). As indicated by the data shown in Fig. 1, differentiation of the cells towards monocytes or neutrophils appears to diminish the abundance of this mRNA. In contrast, expression of the C5a receptor is increased by treatment with dibutyryl-cAMP (16).

Northern blots generated using RNAs from a number of guinea pig tissues, including lung, indicate that the guinea pig PAF receptor cDNA hybridizes with mRNAs of 2.2, 3.0, and 4.0 kb (13). Northern blots of human lung RNA, in contrast, show only a single hybridizing transcript at 4 kb, the same size as obtained with U937 cells (Fig. 1). Size fractionation of the guinea pig RNAs by sucrose density gradient centrifugation followed by expression in *Xenopus* oocytes indicated that the 3.0-kb transcript encodes a functional PAF receptor (13). The human PAF receptor mRNA, however, appears closest in size to the largest of the guinea pig transcripts. It is possible that the lack of expression of the 2.2- and 4.0-kb transcripts in the oocyte relates to mRNA stability or structure, or that

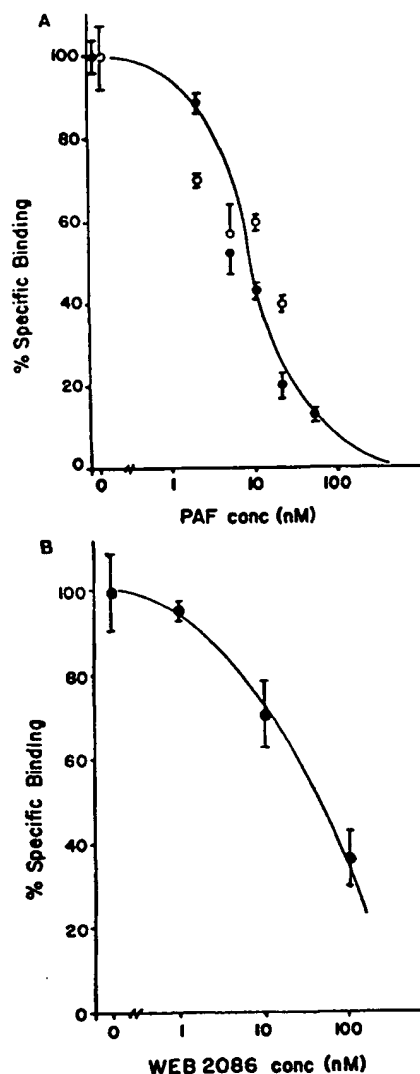


FIG. 5. A, binding of ^3H -labeled PAF to transfected COS-7 cells. pCS1-transfected COS-7 cells (closed circles) or Flag-PAF receptor/pCDM8-transfected cells (open circles) were incubated with 2 nM ^3H -labeled PAF and increasing concentrations of unlabeled PAF as described under "Experimental Procedures." The apparent K_d values by Scatchard analyses are presented in Table I. B, binding was competed effectively by the PAF receptor antagonist WEB2086. Each point represents the mean of duplicate determinations. Nonspecific binding was determined in the presence of 10 μM PAF.

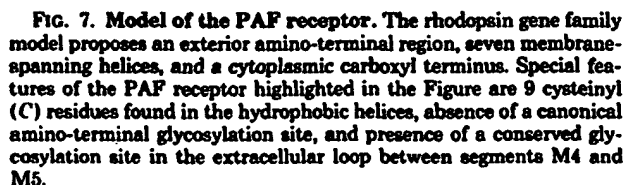
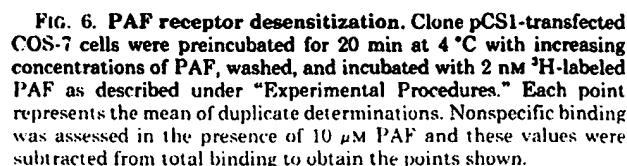
TABLE I
Binding parameters of the human PAF and Flag-PAF receptors transfected in COS-7 cells

Values for K_d and B_{max} were determined from Scatchard analyses of displacement of binding data for each of the constructs transfected into COS-7 cells as described under "Experimental Procedures."

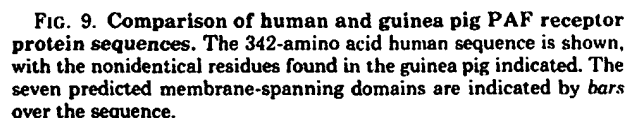
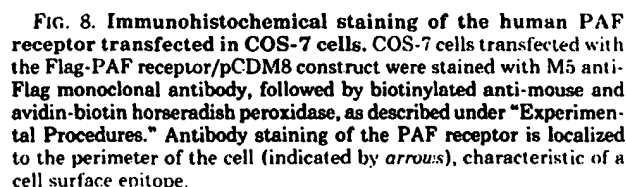
	Temperature °C	K_d nM	B_{max} fmol/dish
PAF	4	5.6	387
	22	5.3	2350
Flag-PAF	22	13.5	2654

the PAF receptor mRNA processing is different in guinea pigs and humans.

Southern blot analysis (Fig. 2) indicates that the human PAF receptor gene exists in a single copy. A similar result



Analysis of the deduced amino acid sequence of the human PAF receptor, as noted previously, indicates seven hydrophobic sequences alternating with more polar regions, characteristic of the seven membrane spanning protein members of the



Unique to the human PAF receptor among this class of molecules is the absence of an *N*-linked glycosylation site in the NH₂-terminal putative extracellular sequence (25). As noted previously, an *N*-linked glycosylation site occurs at positions 169–171, as it does in the guinea pig, in the putative third extracellular loop. A second glycosylation site exists at positions 333–335, in the COOH-terminal cytoplasmic tail, although this position may not be glycosylated because of its presumed intracellular location. The presence of 12 cysteine residues is also unusual for G-protein coupled receptors. Two of these residues are found in conserved positions in the first and second extracellular loops. By analogy with rhodospin (28), a disulfide bond should link residues 90 and 173. Nine of the remaining 10 cysteine residues are found in putative membrane-spanning segments. Ng and Wong (29) have reported that thiol titrants such as para-chloromercuribenzoate and *N*-ethyl maleimide are capable of altering the affinity of

PAF binding to its receptor. Taken together, these data suggest that there may be free thiol groups in the membrane pore created by the seven transmembrane segments and suggest a potential approach to mapping the PAF-binding site.

Another novel feature in the predicted primary structure of the human PAF receptor is the replacement of a highly conserved asparagine residue in the seventh membrane-spanning segment by aspartic acid. In nearly all G-protein-coupled rhodopsin family receptors reported to date, this asparagine residue is part of a ubiquitous region with the sequence NPXXY; indeed, we have previously exploited this homology to clone the human C5a receptor cDNA (16). Interestingly, the only other reported sequence containing an aspartic acid instead of an asparagine at this position occurs in the thromboxane A₂ receptor (30). As these are the only two lipid receptors of this family whose sequences are known to date, we aligned the thromboxane A₂ and PAF sequences and observed that while the protein sequences are only 19% identical, the nucleotide sequences are 50% identical. Therefore, it is conceivable that these sequences may define a new subclass of the rhodopsin family, and may be useful in low stringency screening to identify receptors for other lipid mediators, including the leukotrienes and prostaglandins.

The ligand-binding properties of the human PAF receptor, expressed in COS-7 cells, are similar to those observed using platelets and neutrophils. The K_d for the human platelet PAF receptor was reported by Hwang *et al.* (5) as 4.9 nM, compared with 5.3 nM for the transfected molecule (Table I), and similar to that reported for the cloned guinea pig receptor also expressed in COS-7 cells (13). Uptake of radiolabeled ligand by the receptor at 4 °C on intact COS cells (Fig. 4) was somewhat slower than that observed previously using platelet membranes (5). This may reflect the use of intact cells in our experiments. The PAF receptor antagonist, WEB2086, blocks ³H-labeled PAF binding, as it does for the guinea pig molecule (13), with an ED₅₀ of 5×10^{-6} M.

Additionally, we find 8- to 10-fold higher apparent binding sites per cell when studies are performed at 22 °C instead of at 4 °C (Table I). This may reflect receptor-dependent metabolism of the ligand as described by Homma *et al.* (31), and by Tokumura *et al.* (32). Uptake is exquisitely sensitive to pre-exposure to PAF, since a 20-min treatment at 4 °C with 1 nM PAF, which results in occupancy of only ~10% of the available receptor sites, blocks subsequent binding of radiolabeled ligand by at least 70%. These findings may reflect internalization of the ligand-receptor complex or some other modification of the receptor (e.g. phosphorylation) which renders it unavailable for ligand binding. Indeed, the PAF receptor expressed in COS cells may be a useful system in which to study cellular utilization of PAF as facilitated by its receptor, since no significant uptake occurs on untransfected cells and nonspecific binding is very low.

Because of the utility of the Flag sequence in detection and purification of the C5a anaphylatoxin made in *E. coli* (20), we constructed a Flag-PAF expression plasmid with pCDM8. When transfected into COS-7 cells, the M5 monoclonal antibody, which recognizes the amino acid sequence MDYK-DDDDKEF, was used to localize the epitope to the extracellular surface, providing additional support for the rhodopsin-based model for this class of molecules. Previous support of this structure has only been provided by the β -adrenergic receptor, in which a similar approach was utilized (33). This construct should also be useful for studies of ligand-induced changes in receptor localization. Preliminary experiments indicate that PAF pretreatment appears to cause available

epitopes to polarize to one end of the cell. Additional experiments using appropriately labeled secondary antibodies or protein A can be used to extend these studies to examine such phenomena as ligand-induced metabolism of the receptor and purification of the receptor protein.

Acknowledgment—We thank Dr. Peter F. Weller, Harvard Medical School, for assistance with the immunohistochemical techniques.

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results of BLAST

BLASTN 2.2.8 [Jan-05-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1079535895-1755-55097089079.BLASTQ3

Query=

(1860 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)

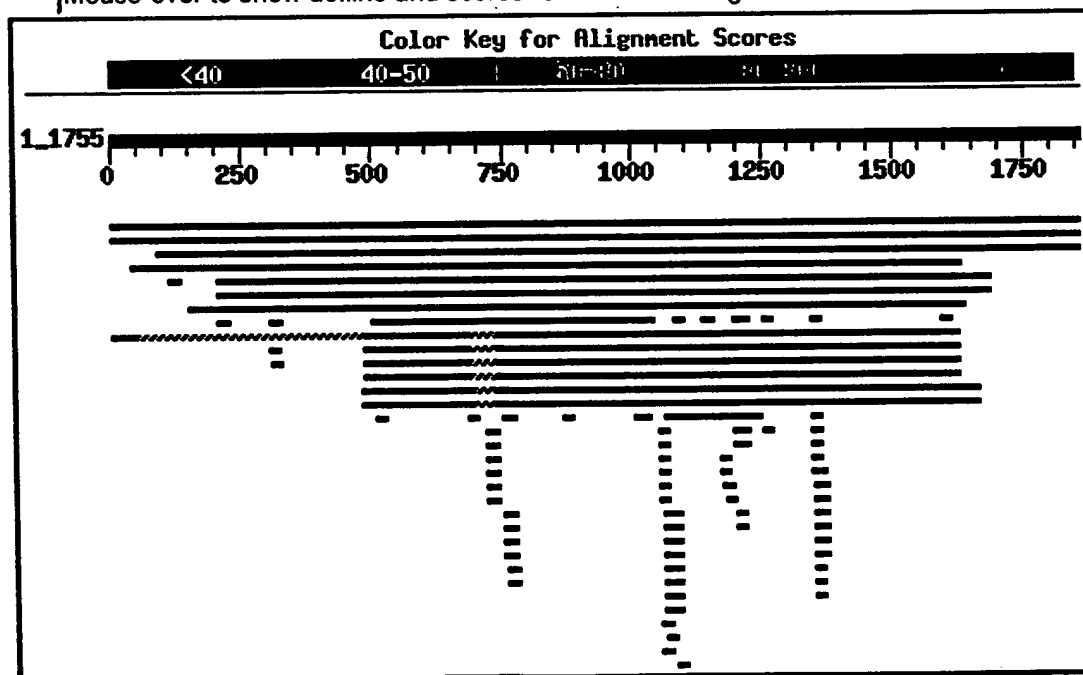
2,102,977 sequences; 10,130,642,339 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 91 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:		Score (bits)	E Value	
gi 13159911 emb AL159140.4 CNS01RGP	Human chromosome 14 DNA...	<u>3663</u>	0.0	
gi 15282112 emb AL162471.3 CNS01RHU	Human chromosome 14 DNA...	<u>3640</u>	0.0	
gi 34190130 gb BC032831.2 	Homo sapiens cDNA clone MGC:2673...	<u>3489</u>	0.0	LU
gi 21928412 dbj AB065563.1 	Homo sapiens gene for seven tra...	<u>3128</u>	0.0	L
gi 32165519 gb AY288418.1 	Homo sapiens G protein-coupled r...	<u>2920</u>	0.0	LU
gi 32261308 ref NM_022571.3 	Homo sapiens G protein-coupled...	<u>2920</u>	0.0	LUG
gi 2810988 gb M76676.1 HUMNP1IY20	Homo sapiens leukocyte pl...	<u>2700</u>	0.0	LUG
gi 29611577 gb AY255588.1 	Homo sapiens leukocyte platelet-...	<u>1082</u>	0.0	LU
gi 38565931 gb BC062104.1 	Mus musculus cDNA clone IMAGE:68...	<u>803</u>	0.0	L
gi 32165533 gb AY288425.1 	Mus musculus G protein-coupled r...	<u>803</u>	0.0	LU
gi 32964966 gb AC110170.6 	Mus musculus chromosome 12, clon...	<u>803</u>	0.0	
gi 32306523 ref NM_181752.1 	Mus musculus G protein-coupled...	<u>803</u>	0.0	LU
gi 32165543 gb AY288430.1 	Rattus norvegicus G protein-coup...	<u>783</u>	0.0	LU
gi 32401462 ref NM_181771.1 	Rattus norvegicus G protein-co...	<u>783</u>	0.0	LU
gi 32563165 emb BX004994.6 	Zebrafish DNA sequence from clo...	<u>137</u>	9e-29	
gi 6031165 ref NM_001480.2 	Homo sapiens galanin receptor 1...	<u>46</u>	0.25	LUG
gi 24648696 ref NM_169955.1 	Drosophila melanogaster CG1082...	<u>46</u>	0.25	LU
gi 24648694 ref NM_142709.1 	Drosophila melanogaster CG1082...	<u>46</u>	0.25	LU
gi 34895453 ref NM_184181.1 	Oryza sativa (japonica cultiva...	<u>46</u>	0.25	U
gi 33589379 gb BT009988.1 	Drosophila melanogaster RE47636 ...	<u>46</u>	0.25	
gi 14090356 dbj AP003233.3 	Oryza sativa (japonica cultivar...	<u>46</u>	0.25	
gi 21629409 gb AC100863.2 	Homo sapiens chromosome 18, clon...	<u>46</u>	0.25	
gi 23171864 gb AE003734.2 	Drosophila melanogaster chromoso...	<u>46</u>	0.25	L
gi 25140120 gb AC096709.19 	Homo sapiens chromosome 18, clo...	<u>46</u>	0.25	
gi 17861010 gb AC008308.8 	Drosophila melanogaster, chromos...	<u>46</u>	0.25	
gi 16258972 gb AC008309.7 	Drosophila melanogaster, chromos...	<u>46</u>	0.25	
gi 44355566 gb AY541036.1 	Homo sapiens galanin receptor 1 ...	<u>46</u>	0.25	
gi 3064071 gb U90658.1 HSGALNRS1	Homo sapiens galanin recep...	<u>46</u>	0.25	L
gi 1297337 gb U53511.1 HSU53511	Homo sapiens galanin recept...	<u>46</u>	0.25	LU
gi 775209 gb U23854.1 HSU23854	Human galanin receptor mRNA,...	<u>46</u>	0.25	LU
gi 559047 gb L34339.1 HUMGALAREC	Human galanin receptor mRN...	<u>46</u>	0.25	LU
gi 12328514 dbj AP002909.2 	Oryza sativa (japonica cultivar...	<u>46</u>	0.25	
gi 22296778 gb AC121870.2 	Mus musculus BAC clone RP24-121D...	<u>44</u>	0.98	
gi 13677146 gb AC013726.7 	Homo sapiens BAC clone RP11-400N...	<u>44</u>	0.98	
gi 29609103 dbj AP005043.1 	Streptomyces avermitilis genomi...	<u>44</u>	0.98	
gi 5001541 gb AC005520.2 AC005520	Homo sapiens PAC clone RP...	<u>44</u>	0.98	
gi 21212029 emb AL662811.20 	Mouse DNA sequence from clone ...	<u>44</u>	0.98	
gi 33457241 gb AC127554.4 	Mus musculus BAC clone RP24-323K...	<u>42</u>	3.9	
gi 21618432 gb BC032702.1 	Homo sapiens G protein-coupled r...	<u>42</u>	3.9	LUG
gi 28630143 gb AC124170.3 	Mus musculus BAC clone RP23-155H...	<u>42</u>	3.9	
gi 38089509 ref XM_357908.1 	Mus musculus similar to SON pr...	<u>42</u>	3.9	LU
gi 37533899 ref NM_196270.1 	Oryza sativa (japonica cultiva...	<u>42</u>	3.9	U
gi 23325376 gb AE014636.1 	Bifidobacterium longum NCC2705 s...	<u>42</u>	3.9	
gi 32567975 gb AC105258.2 	Oryza sativa (japonica cultivar-...	<u>42</u>	3.9	
gi 31431814 gb AE017089.1 	Oryza sativa (japonica cultivar-...	<u>42</u>	3.9	
gi 24418066 gb AC009108.10 	Homo sapiens chromosome 16 clon...	<u>42</u>	3.9	
gi 44886087 dbj AB164051.1 	Oryzias latipes cGK I beta mRNA...	<u>42</u>	3.9	
gi 44886085 dbj AB164050.1 	Oryzias latipes cGK I alpha mRN...	<u>42</u>	3.9	
gi 29366932 gb AC009033.10 	Homo sapiens chromosome 16 clon...	<u>42</u>	3.9	

gi 13424739 gb AE005972.1	Caulobacter crescentus CB15 sect...	42	3.9	
gi 21108849 gb AE011898.1	Xanthomonas axonopodis pv. citri...	42	3.9	
gi 21108642 gb AE011876.1	Xanthomonas axonopodis pv. citri...	42	3.9	
gi 21115400 gb AE012537.1	Xanthomonas campestris pv. campe...	42	3.9	
gi 21741993 emb AL662970.2 OSJN00174	Oryza sativa genomic D...	42	3.9	
gi 32975800 dbj AK065782.1	Oryza sativa (japonica cultivar...	42	3.9	U
gi 18057076 gb AC024591.4	Homo sapiens chromosome 16 clone...	42	3.9	
gi 29609643 dbj AP005045.1	Streptomyces avermitilis genomi...	42	3.9	
gi 455487 dbj D21062.1 MUSGPCR21	Mus musculus GPCR21 mRNA f...	42	3.9	LUG
gi 22531332 emb AJ420781.1 XLA420781	Xenopus laevis mRNA fo...	42	3.9	LU
gi 1545939 emb X94402.1 FRCB1B	F.rubripes CB1B gene for can...	42	3.9	
gi 1890580 emb Z79692.1 RMEXPGNS	R.meliloti exp gene cluster	42	3.9	
gi 15140691 emb AL603645.1 RME603645	Rhizobium meliloti (Si...	42	3.9	
gi 24418991 emb AL939105.1 SCO939105	Streptomyces coelicolo...	42	3.9	
gi 5679837 emb AJ243961.1 OSA243961	Oryza sativa chromosome...	42	3.9	
gi 6634702 emb AJ131718.1 ZMA131718	Zea mays mRNA for legum...	42	3.9	U
gi 17430467 emb AL646076.1	Ralstonia solanacearum GMI1000 ...	42	3.9	
gi 1834557 emb Z84846.1 HSZ84846	H.sapiens gene encoding im...	42	3.9	
gi 1834538 emb Z84827.1 HSZ84827	H.sapiens gene encoding im...	42	3.9	
gi 13625390 gb AF346834.1 AF346834	Mus musculus forkhead pr...	42	3.9	L
gi 4902626 emb AL033397.7 HS27K12	Human DNA sequence from c...	42	3.9	
gi 10444099 gb AF283762.1 AF283762	Mus musculus mouse-thyro...	42	3.9	LUG
gi 10140611 gb AC078839.4 AC078839	Genomic Sequence For Ory...	42	3.9	
gi 12706033 gb AY022817.1	Oryza sativa microsatellite MRG5...	42	3.9	
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gi 16605732 emb AL591003.16	Mouse DNA sequence from clone ...	42	3.9	
gi 10334464 emb AL355296.12	Human DNA sequence from clone ...	42	3.9	
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gi 6465842 emb AL096774.9 HSDJ144C9	Human DNA sequence from...	42	3.9	L
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gi 8218068 emb AL078590.28 HSA557H15	Human DNA sequence fro...	42	3.9	
gi 602311 gb L32831.1 HUMGPCRD	Homo sapiens G protein-coupl...	42	3.9	LG
gi 31377791 ref NM_005281.2	Homo sapiens G protein-coupled...	42	3.9	LUG
gi 21738486 emb AL671858.6	Mouse DNA sequence from clone R...	42	3.9	
gi 18875347 ref NM_133202.1	Mus musculus thyrotropin relea...	42	3.9	LU

Alignments

>gi|13159911|emb|AL159140.4|CNS01RGP **D** Human chromosome 14 DNA sequence BAC R-131E
chromosome 14 of Homo sapiens (Human), complete sequence
Length = 164452

Score = 3663 bits (1848), Expect = 0.0
Identities = 1775/1860 (95%)
Strand = Plus / Minus

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Query: 781 gcttcggcatcgtgtccacgctcagcgtggcgctcatctcgttggaccgttactgcgcta 840

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Sbjct: 128347 tcgtgcggccgcccgggagaagatcgccgcccgcgcgtgcagctgctggcggcg 128288

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Sbjct: 127447 | tgatggaagattctgggggagagttgtggatttcataaagccaaacatttaaagctagag 127388

Query: 1801 | acgggggagggttaccactttccccaacataaaagacaatgtcccttcttcaaaag 1860

Sbjct: 127387 | acgggggagggttaccactttccccaacataaaagacaatgtcccttcttcaaaag 127328

>gi|15282112|emb|AL162471.3|CNS01RHU **D** Human chromosome 14 DNA sequence Partial se
library RPCI-11 from chromosome 14 of Homo sapiens
(Human), complete sequence
Length = 149326

Score = 3640 bits (1836), Expect = 0.0
Identities = 1772/1860 (95%)
Strand = Plus / Plus

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Sbjct: 57931 | cgctcctgcgtaaacacgcggttccctcggcaacgctggaacccacgtcaaaggctccgc 57990

Query: 61 | caggtcccagcgaccgccaccctcggccgagcccagctccccgggcgccgctagc 120

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Query: 1741 tgatggaagattctgggggagagttgtggatttcataaagccaaacatttaaagctagag 1800
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Sbjct: 59671 tgatggaagattctgggggagagttgtggatttcataaagccaaacatttaaagctagag 59730

Query: 1801 acgggggaggcttaccactttcccaaacaacataaaagacaatgtcccttcttcaaaaag 1860
|||||
Sbjct: 59731 acgggggaggcttaccactttcccaaacaacataaaagacaatgtcccttcttcaaaaag 59790

>gi|34190130|gb|BC032831.2| **LU** Homo sapiens cDNA clone MGC:26730 IMAGE:4825908, c
Length = 2557

Score = 3489 bits (1760), Expect = 0.0
Identities = 1687/1772 (95%)
Strand = Plus / Plus

Query: 89 gccgagcccagctccccgcgggcgccgctagccccggccccgagccaccactccgacct 148
|||||
Sbjct: 1 gccgagcccagctccccgcgggcgccgctagccccggccccgagccaccactccgacct 60

Query: 149 agcgggccgcccccggtgcgggatgaggagatccgcgggccgcccactgggccccatgga 208
|||||
Sbjct: 61 agcgggccgcccccggtgcgggatgaggagatccgcgggccgcccactgggccccatgga 120

Query: 209 ggagccgcagccgccccgcccaccagcgagcatggccttactgggcagccagcactccgg 268
|||||
Sbjct: 121 ggagccgcagccgccccgcccaccagcgagcatggccttactgggcagccagcactccgg 180

Query: 269 cgccccctccgcgggccggcccacctggcgggacttctccgcgggccacggcgggccgtgct 328
|||||
Sbjct: 181 cgccccctccgcgggccggcccacctggcgggacttctccgcgggccacggcgggccgtgct 240

Query: 329 ctccttcagcaccgtggcgaccgcgcgctggggaacctgagcgacgcaagcgaggcg 388
|||||
Sbjct: 241 ctccttcagcaccgtggcgaccgcgcgctggggaacctgagcgacgcaagcgaggcg 300

Query: 389 cacagctgccgcnn 448
|||||
Sbjct: 301 cacagctgccgctcccgggtggcgggcgcccttggcggggtccggggcagcgcgggaggcg 360

Query: 449 nnnccgctgctgtcgacaggagctgc 508
|||||
Sbjct: 361 ggcgggcggtgaggcgggcgctaggcccggaggcgcgccgctgctgtcgacaggagctgc 420

Query: 509 agtggcgggcccaggcgctcgctcctcctgctcatcttctgctgtctagccttggcaactg 568


```

Sbjct: 421 agtggcggccccaggcgcgtcgctcctcctgctcatcttcctgctgtctagccttggaactg 480
Query: 569 cgcggtgatgggggtgattgtgaagcacccggcagctccgcaccgtcaccaacgccttcat 628
|||||
Sbjct: 481 cgcggtgatgggggtgattgtgaagcacccggcagctccgcaccgtcaccaacgccttcat 540

Query: 629 cctgtcgctgtccctatcggatctgctcacggcgctgctctgctgcccgcgccttctt 688
|||||
Sbjct: 541 cctgtcgctgtccctatcggatctgctcacggcgctgctctgctgcccgcgccttctt 600

Query: 689 ggacctcttcactccgccccgggggttcggcgccctgccgcgcgcgcggggccctggcgcg 748
|||||
Sbjct: 601 ggacctcttcactccgccccgggggttcggcgccctgccgcgcgcgcggggccctggcgcg 660

Query: 749 cttctgcgcgcgcagccgcttcttcagctcgtgcttcggcatcgtgtccacgctcagcgt 808
|||||
Sbjct: 661 cttctgcgcgcgcagccgcttcttcagctcgtgcttcggcatcgtgtccacgctcagcgt 720

Query: 809 ggcgtcatctcgttgaccgttactgcgctatcgtgcggccgcgcgggagaagatcgg 868
|||||
Sbjct: 721 ggcgtcatctcgttgaccgttactgcgctatcgtgcggccgcgcgggagaagatcgg 780

Query: 869 ccgcccgcgcgcgctgcagctgctggcgggcgccctggctgacggccctgggcttctcctt 928
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Sbjct: 781 ccgcccgcgcgcgctgcagctgctggcgggcgccctggctgacggccctgggcttctcctt 840

Query: 929 gccctgggagctgctcggggcgccccgggaactcgcggcggcgagagcttccacggctg 988
|||||
Sbjct: 841 gccctgggagctgctcggggcgccccgggaactcgcggcggcgagagcttccacggctg 900

Query: 989 cctctaccggacctccccggaccccgcgagctggcgcgcccttcagcgtggggctggt 1048
|||||
Sbjct: 901 cctctaccggacctccccggaccccgcgagctggcgcgcccttcagcgtggggctggt 960

Query: 1049 ggtggcctgctacctgctgcccttctgctcatgtgcttctgccactaccacatctgcaa 1108
|||||
Sbjct: 961 ggtggcctgctacctgctgcccttctgctcatgtgcttctgccactaccacatctgcaa 1020

Query: 1109 gacggtgcgcctgtcggacgtgcgcgtgcggccgggtgaacacctaagcgcgcgctgctg 1168
|||||
Sbjct: 1021 gacggtgcgcctgtcggacgtgcgcgtgcggccgggtgaacacctaagcgcgcgctgctg 1080

Query: 1169 cttcttcagcgaggtgcgcacggccaccaccgctcctcatcatgatcgtcttcgtcatctg 1228
|||||
Sbjct: 1081 cttcttcagcgaggtgcgcacggccaccaccgctcctcatcatgatcgtcttcgtcatctg 1140

Query: 1229 ctgctgggggcccatactgttctcctgggtgctgctggcgccgccccggcaggccccagacat 1288

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|||||
Sbjct: 1141 ctgctgggggcccctactgcttctctgggtgctgctggccgcccggcaggcccagaccat 1200

Query: 1289 gcaggccccctcgctcctcagcgtggtggccgtctggctgacctgggccaatggggccat 1348
|||||
Sbjct: 1201 gcaggccccctcgctcctcagcgtggtggccgtctggctgacctgggccaatggggccat 1260

Query: 1349 caaccctgtcatctacgccatccgcaatcccaacatttcgatgctcctagggcgcaaccg 1408
|||||
Sbjct: 1261 caaccctgtcatctacgccatccgcaatcccaacatttcgatgctcctagggcgcaaccg 1320

Query: 1409 cgaggagggctaccggactaggaatgtggacgctttcctgccagccaggggcccggtct 1468
|||||
Sbjct: 1321 cgaggagggctaccggactaggaatgtggacgctttcctgccagccaggggcccggtct 1380

Query: 1469 gcaagccagaagccgcagtcgccttcgaaaccgctatgccaaaccggctgggggcctgcaa 1528
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Sbjct: 1381 gcaagccagaagccgcagtcgccttcgaaaccgctatgccaaaccggctgggggcctgcaa 1440

Query: 1529 caggatgtcctcttccaaccggccagcggagtgccaggggacgtggccatgtgggcccg 1588
|||||
Sbjct: 1441 caggatgtcctcttccaaccggccagcggagtgccaggggacgtggccatgtgggcccg 1500


Query: 1589 caaaaatccagttgtacttttctgccgagagggaccaccagagccggtgacggcagtgac 1648
|||||
Sbjct: 1501 caaaaatccagttgtacttttctgccgagagggaccaccagagccggtgacggcagtgac 1560

Query: 1649 caaacagcctaaatccgaagctggggataccagcctctaagacggttggaatggccagct 1708
|||||
Sbjct: 1561 caaacagcctaaatccgaagctggggataccagcctctaagacggttggaatggccagct 1620

Query: 1709 tatgaaggcaaatttccactcgcattatttaatgatggaagattctgggggagagttgtg 1768
|||||
Sbjct: 1621 tatgaaggcaaatttccactcgcattatttaatgatggaagattctgggggagagttgtg 1680

Query: 1769 gatttcataaagccaaacattttaaagctagagacgggggaggcttaccactttcccaaa 1828
|||||
Sbjct: 1681 gatttcataaagccaaacattttaaagctagagacgggggaggcttaccactttcccaaa 1740

Query: 1829 caacataaaagacaatgtcccttcttcaaaaag 1860
|||||
Sbjct: 1741 caacataaaagacaatgtcccttcttcaaaaag 1772
```

>gi|21928412|dbj|AB065563.1|  Homo sapiens gene for seven transmembrane helix rec
cds, isolate:CBRC7TM_126
Length = 1590

Score = 3128 bits (1578), Expect = 0.0

Identities = 1505/1590 (94%)
Strand = Plus / Plus

Query: 40 aaccacgtcaaaggctccgccaggtccccagcgaccgccaccctccggccgagcccag 99
|
Sbjct: 1 aaccacgtcaaaggctccgccaggtccccagcgaccgccaccctccggccgagcccag 60

Query: 100 ctccccgcgggcgccgctagccccggccccgagccaccactccgacctagcgggccgccc 159
|
Sbjct: 61 ctccccgcgggcgccgctagccccggccccgagccaccactccgacctagcgggccgccc 120

Query: 160 cccccggtgcgggatgaggagatccgcggccgcccactgggccccatggaggagccgcagc 219
|
Sbjct: 121 cccccggtgcgggatgaggagatccgcggccgcccactgggccccatggaggagccgcagc 180

Query: 220 cgccccgcccaccagcgagcatggccttactgggcagccagcactccggcgccccctccg 279
|
Sbjct: 181 cgccccgcccaccagcgagcatggccttactgggcagccagcactccggcgccccctccg 240

Query: 280 cggccggcccacctggcgggacttcctccgcggccacggcgccgctgctctccttcagca 339
|
Sbjct: 241 cggccggcccacctggcgggacttcctccgcggccacggcgccgctgctctccttcagca 300

Query: 340 ccgtggcgaccgcggcgctggggaacctgagcgacgcaagcggaggcgccacagctgccg 399
|
Sbjct: 301 ccgtggcgaccgcggcgctggggaacctgagcgacgcaagcggaggcgccacagctgccg 360

Query: 400 cnn 459
|
Sbjct: 361 ctcccggtggcgggcgcccttggcggggtccggggcagcgcgggaggcgggggcgcggtga 420

Query: 460 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnccgctgctgtcgcacggagctgcagtggcgggccc 519
|
Sbjct: 421 ggcggccgctaggcccgaggcgggcgccgctgctgtcgcacggagctgcagtggcgggccc 480

Query: 520 aggcgctcgtcctcctgctcatcttctgctgtctagccttggaactgcgcggtgatgg 579
|
Sbjct: 481 aggcgctcgtcctcctgctcatcttctgctgtctagccttggaactgcgcggtgatgg 540

Query: 580 ggggtgattgtgaagcaccggcagctccgcaccgtcaccaacgccttcacctgtcgtgt 639
|
Sbjct: 541 ggggtgattgtgaagcaccggcagctccgcaccgtcaccaacgccttcacctgtcgtgt 600

Query: 640 ccctatcgatctgctcacggcgctgctctgcctgcccgcgccttcttgacctcttca 699
|
Sbjct: 601 ccctatcgatctgctcacggcgctgctctgcctgcccgcgccttcttgacctcttca 660

Query: 700 ctccgcccgggggttcggcgccctgccgcgcgcggggccctggcgcggttctgcgccc 759

0714517004

|||||
Sbjct: 1381 accggactaggaatgtggacgctttcctgccagccagggcccggtctgcaagccagaa 1440

Query: 1480 gccgcagtcgccttcgaaaccgctatgccaaaccggctgggggcctgcaacaggatgtcct 1539
|||||

Sbjct: 1441 gccgcagtcgccttcgaaaccgctatgccaaaccggctgggggcctgcaacaggatgtcct 1500

Query: 1540 cttccaaccggccagcggagtggcaggggacgtggccatgtggggcccgcaaaaatccag 1599
|||||

Sbjct: 1501 cttccaaccggccagcggagtggcaggggacgtggccatgtggggcccgcaaaaatccag 1560

Query: 1600 ttgtacttttctgccgagagggaccaccag 1629
|||||

Sbjct: 1561 ttgtacttttctgccgagagggaccaccag 1590

>gi|32165519|gb|AY288418.1| **LOC** Homo sapiens G protein-coupled receptor 135 (GPR13)
cds
Length = 1485

Score = 2920 bits (1473), Expect = 0.0
Identities = 1400/1485 (94%)
Strand = Plus / Plus

Query: 204 atggaggagccgcagccgccccgcccaccagcgagcatggccttactgggcagccagcac 263
|||||
Sbjct: 1 atggaggagccgcagccgccccgcccaccagcgagcatggccttactgggcagccagcac 60

Query: 264 tccggcgccccctccgcggccggccccacctggcgggacttcctccgcggccacggcgggcc 323
|||||
Sbjct: 61 tccggcgccccctccgcggccggccccacctggcgggacttcctccgcggccacggcgggcc 120

Query: 324 gtgctctccttcagcaccgtggcgaccgcgcgctggggaacctgagcgacgcaagcgga 383
|||||
Sbjct: 121 gtgctctccttcagcaccgtggcgaccgcgcgctggggaacctgagcgacgcaagcgga 180

Query: 384 ggcggcacagctgccgcnnn 443
|||||
Sbjct: 181 ggcggcacagctgccgctcccgggtggcgggcgcccttggcggggtccggggcagcgcgggag 240

Query: 444 nnnccgctgctgtcgcacgga 503
|||||
Sbjct: 241 gcgggggcgggcggtgaggcgccgctaggcccggaggcgggcgccgctgctgtcgcacgga 300

Query: 504 gctgcagtggcgcccaggcgctcgtcctcctgctcatcttctgctgtctagccttggc 563
|||||
Sbjct: 301 gctgcagtggcgcccaggcgctcgtcctcctgctcatcttctgctgtctagccttggc 360

Query: 564 aactgcgcggtgatgggggtgattgtgaagcaccggcagctccgcaccgtcaccaacgcc 623

```

Sbjct: 361      |||
aactgcgcggtgatgggggtgattgtgaagcaccggcagctccgcaccgtcaccaacgcc 420

Query: 624      ttcatcctgtcgctgtccctatcggatctgctcacggcgctgctctgcctgcccgcgcc 683
|||

Sbjct: 421      ttcatcctgtcgctgtccctatcggatctgctcacggcgctgctctgcctgcccgcgcc 480

Query: 684      ttctggacctcttcaactccgcccgggggttcggcgctgcccgcgccgccccctgg 743
|||

Sbjct: 481      ttctggacctcttcaactccgcccgggggttcggcgctgcccgcgccgccccctgg 540

Query: 744      cgcggttcttgcgcgccagccgcttcttcagctcgtgcttcggcatcgtgtccacgctc 803
|||

Sbjct: 541      cgcggttcttgcgcgccagccgcttcttcagctcgtgcttcggcatcgtgtccacgctc 600

Query: 804      agcgtggcgctcatctcggtggaccgttactgcgctatcgtgcggccgcgcgggagaag 863
|||

Sbjct: 601      agcgtggcgctcatctcggtggaccgttactgcgctatcgtgcggccgcgcgggagaag 660

Query: 864      atcgccgcgcgcgcgcgctgcagctgctggcgggcgccctggctgacggccctgggcttc 923
|||

Sbjct: 661      atcgccgcgcgcgcgcgctgcagctgctggcgggcgccctggctgacggccctgggcttc 720

Query: 924      tccttgccctgggagctgctcggggcgccccgggaactcgcgggcggcagagcttccac 983
|||

Sbjct: 721      tccttgccctgggagctgctcggggcgccccgggaactcgcgggcggcagagcttccac 780

Query: 984      ggctgcctctaccggacctccccggaccccgcgagctgggcgcggccttcagcgtgggg 1043
|||

Sbjct: 781      ggctgcctctaccggacctccccggaccccgcgagctgggcgcggccttcagcgtgggg 840

Query: 1044     ctggtggtggcctgctacctgctgcccttctctgctcatgtgcttctgccactaccacatc 1103
|||

Sbjct: 841      ctggtggtggcctgctacctgctgcccttctctgctcatgtgcttctgccactaccacatc 900

Query: 1104     tgcaagacggtgcgctgtcggacgtgcgcgtgcggccggtgaacacctacgcgcgcgtg 1163
|||

Sbjct: 901      tgcaagacggtgcgctgtcggacgtgcgcgtgcggccggtgaacacctacgcgcgcgtg 960

Query: 1164     ctgcgttcttccagcgaggtgcgcacggccaccaccgtcctcatcatgatcgtcttcgtc 1223
|||

Sbjct: 961      ctgcgttcttccagcgaggtgcgcacggccaccaccgtcctcatcatgatcgtcttcgtc 1020

Query: 1224     atctgctgctgggggcccactactgcttctggtgctgctggccgcgcccccggcaggcccag 1283
|||

Sbjct: 1021     atctgctgctgggggcccactactgcttctggtgctgctggccgcgcccccggcaggcccag 1080

Query: 1284     accatgcaggccccctcgctcctcagcgtggtggccgtctggctgacctgggccaatggg 1343

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02/17/2004

١١٥١٢١٣١٤١٥١٦١٧


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Sbjct: 716 cgccgcccgcgcgtgcagctgctggcgggcgcctggctgacggccctgggcttctccttg 775

Query: 930 ccctgggagctgctcggggcgccccgggaactcgcgggcggcagagcttccacggctgc 989  
|||||

Sbjct: 776 ccctgggagctgctcggggcgccccgggaactcgcgggcgccagagcttccacggctgc 835

Query: 990 ctctaccggacctccccggaccccgcgagctgggcgggccttcagcgtggggctggtg 1049  
|||||

Sbjct: 836 ctctaccggacctccccggaccccgcgagctgggcgggccttcagcgtggggctggtg 895

Query: 1050 gtggcctgctacctgctgcccttctctgctcatgtgcttctgccactaccacatctgcaag 1109  
|||||

Sbjct: 896 gtggcctgctacctgctgcccttctctgctcatgtgcttctgccactaccacatctgcaag 955

Query: 1110 acggtgcgccctgtcggacgtgcgcgtgcggccggtgaacacctacgcgcgctgctgcgc 1169  
|||||

Sbjct: 956 acggtgcgccctgtcggacgtgcgcgtgcggccggtgaacacctacgcgcgctgctgcgc- 1014

Query: 1170 ttcttcagcgaggtgcgcacggccaccaccgtcctcatcatgatcgtcttcgtcatctgc 1229  
|||||

Sbjct: 1015 ttcttcagcgaggtgcgcacggccaccaccgtcctcatcatgatcgtcttcgtcatctgc 1074

Query: 1230 tgctgggggcccctactgcttctggtgctgctggccgcccggcaggcccagaccatg 1289  
|||||

Sbjct: 1075 tgctgggggcccctactgcttctggtgctgctggccgcccggcaggcccagaccatg 1134

Query: 1290 caggccccctcgctcctcagcgtggtggccgtctggctgacctgggccaatggggccatc 1349  
|||||

Sbjct: 1135 caggccccctcgctcctcagcgtggtggccgtctggctgacctgggccaatggggccatc 1194

Query: 1350 aaccctgtcatctacgccatccgcaatcccaacatttcgatgctcctagggcgcaaccgc 1409  
|||||

Sbjct: 1195 aaccctgtcatctacgccatccgcaatcccaacatttcgatgctcctagggcgcaaccgc 1254

Query: 1410 gaggagggctaccggactaggaatgtggacgctttcctgccagccagggcccgggtctg 1469  
|||||

Sbjct: 1255 gaggagggctaccggactaggaatgtggacgctttcctgccagccagggcccgggtctg 1314

Query: 1470 caagccagaagccgcagtcgccttcgaaaccgctatgccaaccggctgggggcctgcaac 1529  
|||||

Sbjct: 1315 caagccagaagccgcagtcgccttcgaaaccgctatgccaaccggctgggggcctgcaac 1374

Query: 1530 aggatgtcctcttccaaccggccagcggagtgccaggggacgtggccatgtgggcccgc 1589  
|||||

Sbjct: 1375 aggatgtcctcttccaaccggccagcggagtgccaggggacgtggccatgtggg-ccgc 1433

Query: 1590 aaaaatccagttgtacttttctgccgagagggaccaccagagccggtga 1638  
|||||

Sbjct: 1434 aaaaatccagttgtacttttctgccgaga-ggaccaccagagccggtga 1481

>gi|29611577|gb|AY255588.1| **LU** Homo sapiens leukocyte platelet-activating factor  
partial cds  
Length = 546

Score = 1082 bits (546), Expect = 0.0  
Identities = 546/546 (100%)  
Strand = Plus / Plus

Query: 498 cacggagctgcagtgccggcccaggcgctcgctcctcctgctcatcttctgctgtctagc 557  
|||||  
Sbjct: 1 cacggagctgcagtgccggcccaggcgctcgctcctcctgctcatcttctgctgtctagc 60

Query: 558 cttggcaactgcgcggtgatgggggtgattgtgaagcaccggcagctccgcaccgtcacc 617  
|||||  
Sbjct: 61 cttggcaactgcgcggtgatgggggtgattgtgaagcaccggcagctccgcaccgtcacc 120

Query: 618 aacgccttcacccctgctcgctgtccctatcgatctgctcacggcgctgctctgcctgcc 677  
|||||  
Sbjct: 121 aacgccttcacccctgctcgctgtccctatcgatctgctcacggcgctgctctgcctgcc 180

Query: 678 gccgccttcctggacctcttcactccgccgggggttcggcgctgcccgcggcgggg 737  
|||||  
Sbjct: 181 gccgccttcctggacctcttcactccgccgggggttcggcgctgcccgcggcgggg 240

Query: 738 ccctggcgcggttctgcgccgagccgcttcttcagctcgctgcttcggcatcggtgcc 797  
|||||  
Sbjct: 241 ccctggcgcggttctgcgccgagccgcttcttcagctcgctgcttcggcatcggtgcc 300

Query: 798 acgctcagcgtagcgctcatctcggtggaccgttactgcgctatcgtagcgccgcccggg 857  
|||||  
Sbjct: 301 acgctcagcgtagcgctcatctcggtggaccgttactgcgctatcgtagcgccgcccggg 360

Query: 858 gagaagatcgccgcccgcgcgctgcagctgctggcgggcgccctggctgacggccctg 917  
|||||  
Sbjct: 361 gagaagatcgccgcccgcgcgctgcagctgctggcgggcgccctggctgacggccctg 420

Query: 918 ggcttctccttgccctgggagctgctcgggcgccccgggaactcgcgggcgagagc 977  
|||||  
Sbjct: 421 ggcttctccttgccctgggagctgctcgggcgccccgggaactcgcgggcgagagc 480

Query: 978 ttccacggctgcctctaccggacctccccggacccccgcgagctggcgcgcccttcagc 1037  
|||||  
Sbjct: 481 ttccacggctgcctctaccggacctccccggacccccgcgagctggcgcgcccttcagc 540

Query: 1038 gtgggg 1043  
|||||

Sbjct: 541 gtgggg 546

>gi|38565931|gb|BC062104.1| **L** Mus musculus cDNA clone IMAGE:6809932, with apparent  
Length = 3076

Score = 803 bits (405), Expect = 0.0

Identities = 771/893 (86%)

Strand = Plus / Plus

Query: 735 gggccctggcgcggttctgcgccgccagccgcttcttcagctcgtgcttcggcatcgtg 794  
|||||

Sbjct: 454 gggccctggcgcgagcttctgcgccgccagccgcttcttcagttcgtgtttcggaaatcgta 513

Query: 795 tccacgctcagcggtggcgctcatctcggtggaccggtactgcgctatcgtgcggccgccc 854  
|||||

Sbjct: 514 tccacgttcagcggtggcgctcatctcggtggaccggtactgcgccatcgtgcggccgccc 573

Query: 855 cgggagaagatcgcccgccgcccgcgctgcagctgctggcgggcccgcctggctgacggcc 914  
|||||

Sbjct: 574 cgggacaagctgggcccggcgccgctgcagctgctggcaggagcgtggttggtgctgcg 633

Query: 915 ctgggcttctccttgccctgggagctgctcgggcgccccgggaactcgcgccggcgccag 974  
|||||

Sbjct: 634 ctgggcttctccttgccctgggacctgctcagggcaccccgaggcccccgctccgcag 693

Query: 975 agcttccacggctgcctctaccggacctccccggaccccgccgagctgggcgccccttc 1034  
|||||

Sbjct: 694 agcttccaccgctgcctttacagaacctccccagacctgcgcagctgggcgtgcgctac 753

Query: 1035 agcgtggggctggtggtggcctgctacctgctgcccttctgctcatgtgcttctgccac 1094  
|||||

Sbjct: 754 agcgtgggactggtggtggcttgccttgccttctactgatgtgttctgccgc 813

Query: 1095 taccacatctgcaagacgggtgcgcctgtcggacgtgcgcgtgcggccggtgaacacctac 1154  
|||||

Sbjct: 814 taccacatctgcaagaccgtgcgcctgtcggacgtgcgcgtgcggccgatgaccacctac 873

Query: 1155 gcgcgctgctgcgcttcttcagcgaggtgcgcacggccaccacgtcctcatcatgatc 1214  
|||||

Sbjct: 874 gcgcgctgctgcgcttcttcagcgaggtgcgcacagccaccacgtgctcatcatgatt 933

Query: 1215 gtcttcgtcatctgctgctgggggccctactgcttctggtgctgctggccgcccggc 1274  
|||||

Sbjct: 934 atctttgtcatgtgctgctgggggccctactgcttctggtgctgctggccgcccggc 993

Query: 1275 caggccagaccatgcaggccccctcgtcctcagcgtggtggcgtctggctgacctgg 1334  
|||||

Sbjct: 994 cagggtcaggccacgcaggctccctcgtgctcaatgtggcggtgtttggctgacctgg 1053

Query: 1335 gccaatggggccatcaaccctgtcatctacgccatccgcaatcccaacatttcgatgctc 1394  
 ||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 1054 gccaatggggctatcaaccggtcatatatgccatccgcaacccaacatttcgatgctc 1113

Query: 1395 ctaggcgcaaccgcgaggagggtaccggactaggaatgtggacgctttcctgccagc 1454  
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 Sbjct: 1114 ctaggacgcaaccgcgaagaagggtacaggactagaaacatggatgcttttttgcctagc 1173

Query: 1455 cagggcccggtctgcaagccagaagccgcagtcgccttcgaaaccgctatgccaaaccgg 1514  
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 Sbjct: 1174 caaggcctaggttttcaagccagaagtcgcaatcgcccttcgaaatggctgtgccaacagg 1233

Query: 1515 ctgggggcctgcaacaggatgtcctcttccaaccggccagcggagtggcaggggacgtg 1574  
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 1234 cttggggcttgagcaggatgccttcttccaaccagctagtgggtcaggaggggaagtg 1293

Query: 1575 gccatgtggggccgcgaaaaatccagttgtacttttctgccgagagggaccacc 1627  
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 1294 gtcatgtgggctcgaaaaatccagttgtgctcttcttcgagaggggtccacc 1346

Score = 260 bits (131), Expect = 9e-66  
 Identities = 185/203 (91%)  
 Strand = Plus / Plus

Query: 486 ccgctgctgtcgacaggagctgcagtgggcgcccaggcgctcgtcctcctgctcatcttc 545  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 223 ccgctgctatggcaggggcagcgggtggcgcccaggcgctcgtgctcctgctcatcttc 282

Query: 546 ctgctgtctagccttggaactgcgcggtgatgggggtgattgtgaagcaccggcagctc 605  
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 Sbjct: 283 ttgctgtctagcctgggcaactgcgcggtgatgggggtgatcgtgaagcatcggcagctg 342

Query: 606 cgcaccgtcaccaacgccttcacatcctgtcgctgtccctatcgatctgctcacggcgctg 665  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 343 cgcacggtcacaaacgccttcacatcctgtcgctgtccctgtcggacctgctcactgcgctg 402

Query: 666 ctctgctgcccgcgccttcct 688  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 403 ctctgctaccgcgcgccttcct 425

>gi|32165533|gb|AY288425.1| **LU** Mus musculus G protein-coupled receptor 135 (Gpr13)  
 cds  
 Length = 1374

Score = 803 bits (405), Expect = 0.0  
 Identities = 771/893 (86%)

Strand = Plus / Plus

Query: 735 gggccctggcgcggttctgcgcgccagccgcttcttcagctcgtgcttcggcatcgtg 794  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 421 gggccctggcgcgagcttctgcgcagccagccgcttcttcagttcgtgttcggaatcgta 480

Query: 795 tccacgctcagcgtggcgctcatctcggtggaccgttactgcgctatcgtgcggccgccc 854  
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Sbjct: 481 tccacgttcagcgtggcgctcatctcgctggaccgtactgcgccatcgtgcggccgccc 540

Query: 855 cgggagaagatcggccgcccgcgcgcgtgcagctgctggcgggcgccctggctgacggcc 914  
||||| ||| | ||||| || ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 541 cgggacaagctgggcccggcgcgcgctgcagctgctggcaggagcgtggttggtgctg 600

Query: 915 ctgggcttctccttgcctgggagctgctcggggcgccccgggaactcgcgccggcgag 974  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 601 ctgggcttctccttgcctgggacctgctcagggcaccgccggagcccccgctccgag 660

Query: 975 agcttccacggctgcctctaccggacctccccggaccgccagctggcgccggccttc 1034  
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Sbjct: 661 agcttccaccgctgcctttacagaacctccccagacctgcgcagctggcgctgcctac 720

Query: 1035 agcgtggggctggtggtggcctgctacctgctgcccttcctgctcatgtgcttctgccac 1094  
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Sbjct: 721 agcgtgggactggtggtggcctgctacttgccttcctactgatgtgttctgccgc 780

Query: 1095 taccacatctgcaagacggtgcgcctgtcggacgtgcgcgtgcggccggtgaacacctac 1154  
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Sbjct: 781 taccacatctgcaagaccgtgcgcctgtcggacgtgcgcgtgcggccgatgaccacttac 840

Query: 1155 gcgcgcgtgctgcgcttcttcagcgaggtgcgcacggccaccaccgtcctcatcatgatc 1214  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 841 gcgcgcgtgctgcgcttcttcagcgaggtgcgcacagccaccaccgtgctcatcatgatt 900

Query: 1215 gtcttcgtcatctgctgctgggggccctactgcttcctggtgctgctggccgcccgg 1274  
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Sbjct: 901 atctttgtcatgtgctgctggggccctactgcttcctggtgctgctggccgcgaccgg 960

Query: 1275 caggcccagaccatgcaggccccctcgtcctcagcgtggtggcgtctggctgacctgg 1334  
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Sbjct: 961 cagggtcaggccacgcaggctccctcgtgctcaatgtggcggtgtttggctgacctgg 1020

Query: 1335 gccaatggggccatcaacctgtcatctacgccatccgcaatcccaacatttcgatgctc 1394  
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Sbjct: 1021 gccaatggggctatcaaccgggtcatatatgccatccgcaaccccaacatttcgatgctc 1080

Query: 1395 ctagggcgcaaccgcgaggagggtaccggactaggaatgtggacgctttcctgccagc 1454  
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Sbjct: 1081 ctaggacgcaaccgcgaagaaggggtacaggactagaaacatggatgcttttttgcctagc 1140

Query: 1455 cagggcccgggtctgcaagccagaagccgcagtcgccttcgaaaccgctatgccaaccgg 1514  
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Sbjct: 1141 caaggcctaggttttcaagccagaagtcgcaatcgcccttcgaaatggctgtgccaacagg 1200

Query: 1515 ctgggggctgcaacaggatgtcctcttccaaccggccagcggagtgccaggggacgtg 1574  
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Sbjct: 1201 cttggggcttgagcaggatgccttcttccaaccagctagtgggtcaggaggggaagtg 1260

Query: 1575 gccatgtggggccgcacaaaatccagttgtacttttctgccgagagggaccacc 1627  
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Sbjct: 1261 gtcatgtgggctcgaaaaaatccagttgtgctcttcttcgagaggggtccacc 1313

Score = 260 bits (131), Expect = 9e-66  
 Identities = 185/203 (91%)  
 Strand = Plus / Plus

Query: 486 ccgctgctgtgcacggagctgcagtgggcgccagggcgtcgtcctcctgctcatcttc 545  
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Sbjct: 190 ccgctgctatggcacggggcagcgggtggccgcccagggcgtcgtgctcctgctcatcttc 249

Query: 546 ctgctgtctagccttggcaactgcgcgggtgatgggggtgattgtgaagcaccggcagctc 605  
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Sbjct: 250 ttgctgtctagcctgggcaactgcgcgggtgatgggggtgatcgtgaagcatcggcagctg 309

Query: 606 cgcaccgtcaccaacgccttcctcctgctcgtgctccctatcgatctgctcacggcgctg 665  
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Sbjct: 310 cgcacggtcacaaacgccttcctcctgctcgtgctccctgctcgacctgctcactgcgctg 369

Query: 666 ctctgcctgcccgcgccttcct 688  
 ||||| ||||| ||||| |||||

Sbjct: 370 ctctgcctaccgcgccttcct 392

>gi|32964966|gb|AC110170.6| **D** Mus musculus chromosome 12, clone RP23-301G24, compl  
 Length = 173081

Score = 803 bits (405), Expect = 0.0  
 Identities = 771/893 (86%)  
 Strand = Plus / Minus

Query: 735 gggccctggcgcggttctgcgcgccagccgcttcttcagctcgtgcttcggcatcgtg 794  
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Sbjct: 35355 gggccctggcgcgagcttctgcgcagccagccgcttcttcagttcgtgtttcgggaatcgta 35296

Query: 795 tccacgctcagcgtggcgctcatctcgttggaccgttactgcgctatcgtgcggccgccc 854  
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Sbjct: 35295 tccacgttcagcgtggcgctcatctcgctggaccgctactgcgccatcgtgcggccgccc 35236

Query: 855 cgggagaagatcggccgccgcccgcgcgtgcagctgctggcgggcgccctggctgacggcc 914  
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Sbjct: 35235 cgggacaagctgggcccggcgcgcgctgcagctgctggcaggagcgtgggttggtgcg 35176

Query: 915 ctgggcttctccttgccctgggagctgctcgggcgccccgggaactcgcggcgccgcag 974  
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Sbjct: 35175 ctgggcttctccttgccctgggacctgctcagggcaccccgaggcccccgctccgcag 35116

Query: 975 agcttccacggctgcctctaccggacctccccggaccccgcgagctgggcgcggccttc 1034  
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Sbjct: 35115 agcttccaccgctgcctttacagaacctcccagacctgcgagctgggcgtcgcttac 35056

Query: 1035 agcgtggggctgggtgggtggcctgctacctgctgcccttctgctcatgtgcttctgccac 1094  
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Sbjct: 35055 agcgtgggactgggtgggtggcttgtacttgccttctactgatgtgttctgccgc 34996

Query: 1095 taccacatctgcaagacgggtgcgcctgtcggacgtgcgcgtgcggccggtgaacacctac 1154  
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Sbjct: 34995 taccacatctgcaagaccgtgcgcctgtcggacgtgcgcgtgcggccgatgaccacttac 34936

Query: 1155 gcgcgcgtgctgcgcttcttcagcgaggtgcgcacggccaccacgctcctcatcatgac 1214  
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Sbjct: 34935 gcgcgcgtgctgcgcttcttcagcgaggtgcgcacagccaccacgctgctcatcatgatt 34876

Query: 1215 gtcttcgtcatctgctgctgggggccctactgcttcctgggtgctgctggccgcccggc 1274  
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Sbjct: 34875 atctttgtcatgtgctgctggggccctactgcttcctgggtgctgctggccgcgacccgg 34816

Query: 1275 caggcccagaccatgcaggccccctcgctcctcagcgtgggtggccgtctggctgacctgg 1334  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 34815 cagggtcaggccacgcaggctccctcgctgctcaatgtggcggctgtttggctgacctgg 34756

Query: 1335 gccaatggggccatcaaccctgtcatctacgccatccgcaatcccaacatttcgatgctc 1394  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 34755 gccaatggggctatcaaccgggtcatatatgccatccgcaaccccaacatttcgatgctc 34696

Query: 1395 ctaggcgcaaccgcgaggagggtaccggactaggaatgtggacgctttctgccagc 1454  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 34695 ctaggacgcaaccgcgaagaagggtacaggactagaaacatggatgctttttgcctagc 34636

Query: 1455 caggggccgggtctgcaagccagaagccgcagtcgccttcgaaaccgctatgccaaccgg 1514  
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Sbjct: 34635 caaggcctaggttttcaagccagaagtcgcaatcgcccttcgaaatggctgtgccaacagg 34576

Query: 1515 ctgggggcctgcaacaggatgtcctcttccaaccggccagcggagtgccaggggacgtg 1574  
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Sbjct: 34575 cttggggcttgacgacgagatgccttcttccaacccagctagtgggtcaggaggggaagtg 34516

Query: 1575 gccatgtgggcccgcacaaaatccagttgtacttttctgccgagagggaccacc 1627

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Sbjct: 34515 gtcattgtgggtcgcacaaaatccagttgtgctcttcttccgagaggggtccacc 34463

Score = 260 bits (131), Expect = 9e-66

Identities = 185/203 (91%)

Strand = Plus / Minus

Query: 486 ccgctgctgtcgcacggagctgcagtggcgccaggcgctcgtcctcctgctcatcttc 545

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Sbjct: 35586 ccgctgctatggcacggggcagcgggtggccgcccaggcgctcgtgctcctgctcatcttc 35527

Query: 546 ctgctgtctagccttggcaactgcgcggtgatgggggtgattgtgaagcaccggcgagctc 605

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Sbjct: 35526 ttgctgtctagcctgggcaactgcgcggtgatgggggtgatcgtgaagcatcggcagctg 35467

Query: 606 cgcaccgtcaccaacgccttcctcctgtcgtgtccctatcgatctgctcacggcgctg 665

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Sbjct: 35466 cgcacgggtcacaacgccttcctcctgtcgtgtccctgtcggacctgctcactgcgctg 35407

Query: 666 ctctgcctgcccgcgcgcttct 688

||||| ||||| ||||| |||||

Sbjct: 35406 ctctgcctaccgcgcgcttct 35384

Score = 58.0 bits (29), Expect = 7e-05

Identities = 45/49 (91%), Gaps = 1/49 (2%)

Strand = Plus / Minus

Query: 4 tcctgcgtaaacacgcggttccctcggcaacgc-tggaaccacgtcaa 51

||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 35943 tcctgcgtaaataggcggttccctcggcaacgcctagaaccacgtcaa 35895

>gi|32306523|ref|NM\_181752.1| **LU** Mus musculus G protein-coupled receptor 135 (Gpr  
Length = 1374

Score = 803 bits (405), Expect = 0.0

Identities = 771/893 (86%)

Strand = Plus / Plus

Query: 735 gggccctggcgcggttctctgcgcgccagccgcttcttcagctcgtgcttcggcatcgtg 794

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Sbjct: 421 gggccctggcgcgagcttctgcgcagccagccgcttcttcagttcgtgttcggaatcgta 480

Query: 795 tccacgctcagcgtggcgctcatctcgttggaccgttactgcgctatcgtgcggccgccc 854

03/17/2004

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 Sbjct: 1201 cttggggcttgagcaggatgccttcttccaaccagctagtgggtcaggaggggaagtg 1260

Query: 1575 gccatgtgggcccgcacaaatccagttgtacttttctgccgagagggaccacc 1627

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 Sbjct: 1261 gtcatgtgggctcgacaaatccagttgtgctcttctccgagaggggtccacc 1313

Score = 260 bits (131), Expect = 9e-66  
 Identities = 185/203 (91%)  
 Strand = Plus / Plus

Query: 486 ccgctgctgtcgcacggagctgcagtggcgccagcgctcgtcctcctgctcatcttc 545

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 Sbjct: 190 ccgctgctatggcacggggcagcggtggcgccagcgctcgtgctcctgctcatcttc 249

Query: 546 ctgctgtctagccttggcaactgcgcggtgatgggggtgattgtgaagcaccggcagctc 605

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 Sbjct: 250 ttgctgtctagcctgggcaactgcgcggtgatgggggtgatcgtgaagcatcggcagctg 309

Query: 606 cgcaccgtcaccaacgccttcctcctgctcgtgctccctatcggtatctgctcacggcgctg 665

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 Sbjct: 310 cgcacgggtcacaacgccttcctcctgctcgtgctccctgctcggaacctgctcactgcgctg 369

Query: 666 ctctgcctgcccgcgccttct 688

||||| ||||| ||||| |||||  
 Sbjct: 370 ctctgcctacccgcgccttct 392

>[gi|32165543|gb|AY288430.1|](#) **LU** Rattus norvegicus G protein-coupled receptor 135 (complete cds)  
 Length = 1374

Score = 783 bits (395), Expect = 0.0  
 Identities = 797/931 (85%)  
 Strand = Plus / Plus

Query: 733 cggggccctggcgcggttctgcgccgccagccgcttcttcagctcgtgcttcggcatcg 792

||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 419 cggggccctggcgagcttctgcgccgccagccgcttcttcagttcgtgtttcggcatcg 478

Query: 793 tgtccacgctcagcgtggcgctcatctcgttgaccgttactgcgctatcgtgcggccgc 852

| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 479 tctccacgttcagcgtggcgctcatctcgttgaccgttactgcgcatcgtgcggccgc 538

Query: 853 cgcgggagaagatcgccgcgcgcgcgcgcgtgcagctgctggcgggcgccctggctgacgg 912

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 Sbjct: 539 cgcgggacaagctaggccggcgcgcgctgcagctgctggcgggagcgtggctggctg 598

02/17/2024

```
Query: 1633 cggtgacggcagtgaccaaacagcctaaatc 1663
          | | | | | | | | | | | | | | | |
Sbjct: 1319 cagttatggcagtcacaaacagcataaatc 1349
```

Score = 258 bits (130), Expect = 3e-65  
Identities = 189/214 (88%)  
Strand = Plus / Plus

Query: 481 nnnnnccgctgctgtcgcacggagctgcagtggcgggccagggcgctcgtcctcctgctca 540  
 ||||| | ||||| || ||||| ||||| ||||| ||||| |||||  
 Sbjct: 185 cggcaccgctgctttggcacggggcagcagtggccgcccagggcgctcgtgctcctgctca 244

Query: 541 tcttctgctgtctagccttggcaactgcgcggtgatgggggtgattgtgaagcaccggc 600  
 ||||| | ||||||||| || ||||||||| ||||||||| |||||||||  
 Sbjct: 245 tcttcttactgtctagcctgggaaactgcgcggtgatgggggtgatcgtgaagcaccggc 304

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Query: 601 agctccgcaccgtcaccaacgccttcacctgtcgctgtccctatcggatctgctcacgg 660
          |||| | |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |
Sbjct: 305 agctgcgacaggtcaccaacgccttcacctatcgctgtccctgtcggacctgctcactg 364
```

```
Query: 661 cgctgctctgcctgccggccgccttcctggacct 694  
      ||||| |  
Sbjct: 365 cgctgctctgcttaccggccgccttcctcgacct 398
```

```
>gi|32401462|ref|NM_181771.1| LU Rattus norvegicus G protein-coupled receptor 135
      Length = 1374
```

Score = 783 bits (395), Expect = 0.0  
Identities = 797/931 (85%)  
Strand = Plus / Plus

```
Query: 733 cggggccctggcgcggttctgcgccgacgcgcttcttcagctcgtgcttcggcatcg 792
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 419 cggggccctggcgcggttctgcgccgacgcgcttcttcagtctcgtggttcggcatcg 478
```

```
Query: 793  tgtccacgctcagcgtggcgctcatctcggttgaccggtactgcgctatcgtgcgggcgc 852
          | ||||| |||||||||||||||| ||||| ||||||| ||||||||||||
Sbjct: 479  tctccacgttcagcgtggcgctcatctcgctggaccgctactgcgccatcgtgcgggcgc 538
```

```
Query: 853 cgcgggagaagatcggccgcccgcgcgctgcagctgctggcgggcgcctggctgacgg 912
          ||||| | | |||| | | ||||||| ||||| | | ||||| | |
Sbjct: 539 cgcgggacaagctaggccggcggcgcgcgctgcagctgctggccggagcgtggctggctg 598
```

```
Query: 913 ccctgggcttctccttgccctgggagctgctcggggcgccccgggaactcgcggcggcgc 972
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 599 cgctcggttctccctgccctgggagctgctccgggcacccccgggagccccgactccgc 658
```

```
Query: 1633 cggtgacggcagtgacaaacagcctaaatc 1663
          | | | | | | | | | | | | | | | |
Sbjct: 1319 cagttatggcagtctacaaacagcataaatc 1349
```

Score = 258 bits (130), Expect = 3e-65  
Identities = 189/214 (88%)  
Strand = Plus / Plus

Query: 481 nnnnnccgctgctgtcgacggagctgcagtgggcgccaggcgctcgtcctcctgctca 540  
          ||||||| | ||||| || ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 185 cggcaccgctgctttggcacggggcagcagtgggcgccaggcgctcgtgctcctgctca 244

Query: 541 tcttcctgctgtctagccttggcaactgcgcggtgatgggggtgattgtgaagcaccggc 600  
          |||| | ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 245 tcttcttactgtctagcctgggaaactgcgcggtgatgggggtgatcgtgaagcaccggc 304

Query: 601 agctccgcaccgtcaccaacgccttcctcctgctcctatcggtatctgctcacgg 660  
          |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 305 agctgcgcacggtcaccaacgccttcctcctatcgctgctcctgctcgacactgctcactg 364

Query: 661 cgctgctctgcctgcccgcgccttcctggacct 694  
          ||||||| | ||||| ||||| |||||  
Sbjct: 365 cgctgctctgcttaccgcgccttcctcgacct 398

>gi|32563165|emb|BX004994.6| **D** Zebrafish DNA sequence from clone DKEY-24J15 in lin  
          complete sequence  
          Length = 211945

Score = 137 bits (69), Expect = 9e-29  
Identities = 159/189 (84%)  
Strand = Plus / Minus

Query: 1059 tacctgctgcccttcctgctcatgtgcttctgccactaccacatctgcaagacgggtgcgc 1118  
          ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 94318 tacctgcttccttcgcctcatgtgcttctgccactacaacatctgcaaaacagtcggg 94259

Query: 1119 ctgtcggacgtgcgcgtgcccgggtgaacacctacgcgcgctgctgcgcttcttcagc 1178  
          ||||||| | | ||||| ||||| | || ||||| | || ||||| |||||  
Sbjct: 94258 ctgtcggagatcagggtgcccgggtcaccacttacgcgcacctgttgcgcttctacagc 94199

Query: 1179 gaggtgcgcacggccaccaccgtcctcatcatgatcgtcttcgtcatctgctgctggggg 1238  
          ||| ||||| || ||||| ||||| ||||| || ||| ||||| ||||| |||||  
Sbjct: 94198 gagatgcgcacgcgaccaccgtgctcatcatgattgtgttcagcatcttctgctggggg 94139

Query: 1239 ccctactgc 1247  
          |||||||  
Sbjct: 94138 ccctactgc 94130

>gi|6031165|ref|NM\_001480.2| **LUG** Homo sapiens galanin receptor 1 (GALR1), mRNA  
          Length = 3056



Score = 46.1 bits (23), Expect = 0.25  
Identities = 32/35 (91%)  
Strand = Plus / Plus

Query: 1057 gctacctgctgcccttcctgctcatgtgcttctgc 1091  
|||||||  
Sbjct: 1395 gctacctgctgccgctcctgctcatctgcttctgc 1429

>gi|24648696|ref|NM\_169955.1| **LU** Drosophila melanogaster CG10823-PB [Drosophila m  
(CG10823) mRNA, complete cds  
Length = 1752

Score = 46.1 bits (23), Expect = 0.25  
Identities = 23/23 (100%)  
Strand = Plus / Plus

Query: 1048 tgggtggcctgctacctgctgccc 1070  
|||||||  
Sbjct: 1346 tgggtggcctgctacctgctgccc 1368

>gi|24648694|ref|NM\_142709.1| **LU** Drosophila melanogaster CG10823-PA [Drosophila m  
(CG10823) mRNA, complete cds  
Length = 4523

Score = 46.1 bits (23), Expect = 0.25  
Identities = 23/23 (100%)  
Strand = Plus / Plus

Query: 1048 tgggtggcctgctacctgctgccc 1070  
|||||||  
Sbjct: 1346 tgggtggcctgctacctgctgccc 1368

>gi|34895453|ref|NM\_184181.1| **U** Oryza sativa (japonica cultivar-group) P0037C04.21  
mRNA  
Length = 1020

Score = 46.1 bits (23), Expect = 0.25  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1196 caccgtcctcatcatgatcgtcttcgctcatc 1226  
|||||||  
Sbjct: 991 caccgtcctcatcatcctcgtcttcgctcatc 961

>gi|33589379|gb|BT009988.1| Drosophila melanogaster RE47636 full insert cDNA  
Length = 4808

Score = 46.1 bits (23), Expect = 0.25  
Identities = 23/23 (100%)  
Strand = Plus / Plus

Query: 1048 tggtagcctgctacctgctgccc 1070  
|||||  
Sbjct: 1387 tggtagcctgctacctgctgccc 1409

>[gi|14090356|dbj|AP003233.3](#) **D** Oryza sativa (japonica cultivar-group) genomic DNA,  
clone:P0037C04  
Length = 137879

Score = 46.1 bits (23), Expect = 0.25  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1196 caccgtcctcatcatgatcgtcttcgtcatc 1226  
|||||  
Sbjct: 73349 caccgtcctcatcatcctcgtcttcgtcatc 73319

>[gi|21629409|gb|AC100863.2](#) **D** Homo sapiens chromosome 18, clone RP11-751H17, compl  
Length = 175527

Score = 46.1 bits (23), Expect = 0.25  
Identities = 32/35 (91%)  
Strand = Plus / Plus

Query: 1057 gctacctgctgcccttcctgctcatgtgcttctgc 1091  
|||||  
Sbjct: 141358 gctacctgctgccgctcctgctcatgtgcttctgc 141392

>[gi|23171864|gb|AE003734.2](#) **LID** Drosophila melanogaster chromosome 3R, section 72  
complete sequence  
Length = 241480

Score = 46.1 bits (23), Expect = 0.25  
Identities = 23/23 (100%)  
Strand = Plus / Minus

Query: 1048 tggtagcctgctacctgctgccc 1070  
|||||  
Sbjct: 66542 tggtagcctgctacctgctgccc 66520

>[gi|25140120|gb|AC096709.19](#) **D** Homo sapiens chromosome 18, clone RP11-707P24, comp  
Length = 199285

Score = 46.1 bits (23), Expect = 0.25  
Identities = 32/35 (91%)  
Strand = Plus / Minus

Query: 1057 gctacctgctgcccttcctgctcatgtgcttctgc 1091  
|||||  
Sbjct: 154584 gctacctgctgccgctcctgctcatctgcttctgc 154550

>[gi|17861010|gb|AC008308.8|](#) **D** Drosophila melanogaster, chromosome 3R, region 93C-9  
BACR10M16, complete sequence  
Length = 195868

Score = 46.1 bits (23), Expect = 0.25  
Identities = 23/23 (100%)  
Strand = Plus / Minus

Query: 1048 tgggtggcctgctacctgctgccc 1070  
|||||  
Sbjct: 140664 tgggtggcctgctacctgctgccc 140642

>[gi|16258972|gb|AC008309.7|](#) **D** Drosophila melanogaster, chromosome 3R, region 93D-9  
BACR06L13, complete sequence  
Length = 162770

Score = 46.1 bits (23), Expect = 0.25  
Identities = 23/23 (100%)  
Strand = Plus / Minus

Query: 1048 tgggtggcctgctacctgctgccc 1070  
|||||  
Sbjct: 26083 tgggtggcctgctacctgctgccc 26061

>[gi|44355566|gb|AY541036.1|](#) Homo sapiens galanin receptor 1 mRNA, complete cds  
Length = 1050

Score = 46.1 bits (23), Expect = 0.25  
Identities = 32/35 (91%)  
Strand = Plus / Plus

Query: 1057 gctacctgctgcccttcctgctcatgtgcttctgc 1091  
|||||  
Sbjct: 623 gctacctgctgccgctcctgctcatctgcttctgc 657

>[gi|3064071|gb|U90658.1|HSGALNRS1](#) **L** Homo sapiens galanin receptor (GALNR) gene, ex  
Length = 1796

Score = 46.1 bits (23), Expect = 0.25

Identities = 32/35 (91%)  
Strand = Plus / Plus

Query: 1057 gctacctgctgcccttcctgctcatgtgcttctgc 1091  
||||||| ||||| |||||  
Sbjct: 1721 gctacctgctgccgctcctgctcatctgcttctgc 1755

>gi|1297337|gb|U53511.1|HSU53511 **LU** Homo sapiens galanin receptor (Gall-R) mRNA,  
Length = 1053

Score = 46.1 bits (23), Expect = 0.25  
Identities = 32/35 (91%)  
Strand = Plus / Plus

Query: 1057 gctacctgctgcccttcctgctcatgtgcttctgc 1091  
||||||| ||||| |||||  
Sbjct: 623 gctacctgctgccgctcctgctcatctgcttctgc 657

>gi|775209|gb|U23854.1|HSU23854 **LU** Human galanin receptor mRNA, complete cds  
Length = 1050

Score = 46.1 bits (23), Expect = 0.25  
Identities = 32/35 (91%)  
Strand = Plus / Plus

Query: 1057 gctacctgctgcccttcctgctcatgtgcttctgc 1091  
||||||| ||||| |||||  
Sbjct: 623 gctacctgctgccgctcctgctcatctgcttctgc 657

>gi|559047|gb|L34339.1|HUMGALAREC **LU** Human galanin receptor mRNA, complete cds  
Length = 1053

Score = 46.1 bits (23), Expect = 0.25  
Identities = 32/35 (91%)  
Strand = Plus / Plus

Query: 1057 gctacctgctgcccttcctgctcatgtgcttctgc 1091  
||||||| ||||| |||||  
Sbjct: 623 gctacctgctgccgctcctgctcatctgcttctgc 657

>gi|12328514|dbj|AP002909.2| **D** Oryza sativa (japonica cultivar-group) genomic DNA,  
clone:P0044F08  
Length = 141528

Score = 46.1 bits (23), Expect = 0.25  
Identities = 29/31 (93%)  
Strand = Plus / Minus

Query: 1196 caccgtcctcatcatgatcgtcttcggtcatc 1226  
 |||  
 Sbjct: 24919 caccgtcctcatcatcctcgtcttcggtcatc 24889

>gi|22296778|gb|AC121870.2| **D** Mus musculus BAC clone RP24-121D5 from 9, complete s  
 Length = 191747

Score = 44.1 bits (22), Expect = 0.98  
 Identities = 22/22 (100%)  
 Strand = Plus / Minus

Query: 114 cgctagcccccgccccgagcc 135  
 |||  
 Sbjct: 162779 cgctagcccccgccccgagcc 162758

>gi|13677146|gb|AC013726.7| **D** Homo sapiens BAC clone RP11-400N9 from 2, complete s  
 Length = 214647

Score = 44.1 bits (22), Expect = 0.98  
 Identities = 22/22 (100%)  
 Strand = Plus / Plus

Query: 1059 tacctgctgcccttcctgctca 1080  
 |||  
 Sbjct: 938 tacctgctgcccttcctgctca 959

>gi|29609103|dbj|AP005043.1| **D** Streptomyces avermitilis genomic DNA, complete geno  
 Length = 299925

Score = 44.1 bits (22), Expect = 0.98  
 Identities = 22/22 (100%)  
 Strand = Plus / Minus

Query: 305 ctccgcggccacggcgccgtg 326  
 |||  
 Sbjct: 61594 ctccgcggccacggcgccgtg 61573

>gi|5001541|gb|AC005520.2|AC005520 **D** Homo sapiens PAC clone RP5-1021I20 from 14q24  
 Length = 151123

Score = 44.1 bits (22), Expect = 0.98  
 Identities = 22/22 (100%)  
 Strand = Plus / Plus

Query: 206 ggaggagccgcagcccccgc 227

|||||  
Sbjct: 28563 ggaggagccgcagccgccccgc 28584

>gi|21212029|emb|AL662811.20| **D** Mouse DNA sequence from clone RP23-202E24 on chrom  
sequence  
Length = 226642

Score = 44.1 bits (22), Expect = 0.98  
Identities = 22/22 (100%)  
Strand = Plus / Minus

Query: 1050 gtggcctgctacctgctgccct 1071  
|||||  
Sbjct: 37854 gtggcctgctacctgctgccct 37833

>gi|33457241|gb|AC127554.4| **D** Mus musculus BAC clone RP24-323K23 from chromosome 8  
sequence  
Length = 178416

Score = 42.1 bits (21), Expect = 3.9  
Identities = 21/21 (100%)  
Strand = Plus / Minus

Query: 719 gcctgccgccgccgcggggcc 739  
|||||  
Sbjct: 6735 gcctgccgccgccgcggggcc 6715

>gi|21618432|gb|BC032702.1| **LUG** Homo sapiens G protein-coupled receptor 3, mRNA  
IMAGE:5247608), complete cds  
Length = 2145

Score = 42.1 bits (21), Expect = 3.9  
Identities = 27/29 (93%)  
Strand = Plus / Plus

Query: 1347 atcaaccctgtcatctacgccatccgcaa 1375  
|||||  
Sbjct: 969 atcaaccctatcatctacgccttccgcaa 997

>gi|28630143|gb|AC124170.3| **D** Mus musculus BAC clone RP23-155H5 from 8, complete s  
Length = 235023

Score = 42.1 bits (21), Expect = 3.9  
Identities = 21/21 (100%)  
Strand = Plus / Minus

Query: 719 gcctgccgccgccgcggggcc 739

|||||  
Sbjct: 224800 gcctgccgccgccgccggggcc 224780

>gi|38089509|ref|XM\_357908.1| **LU** Mus musculus similar to SON protein (SON3) (Nega  
element-binding protein) (NRE-binding protein) (DBP-5)  
(Bax antagonist selected in saccharomyces 1) (BASS1)  
(LOC384869), mRNA  
Length = 1047

Score = 42.1 bits (21), Expect = 3.9  
Identities = 21/21 (100%)  
Strand = Plus / Plus

Query: 719 gcctgccgccgccgccggggcc 739  
|||||  
Sbjct: 10 gcctgccgccgccgccggggcc 30

>gi|37533899|ref|NM\_196270.1| **U** Oryza sativa (japonica cultivar-group) Centrin (OS  
mRNA  
Length = 2565

Score = 42.1 bits (21), Expect = 3.9  
Identities = 24/25 (96%)  
Strand = Plus / Minus

Query: 749 cttctgcgccgccagccgcttcttc 773  
|||||  
Sbjct: 135 cttctgcgccgctcagccgcttcttc 111

>gi|23325376|gb|AE014636.1| **D** Bifidobacterium longum NCC2705 section 23 of 202 of  
genome  
Length = 11431

Score = 42.1 bits (21), Expect = 3.9  
Identities = 21/21 (100%)  
Strand = Plus / Plus

Query: 308 cgcgccacggcgccgtgct 328  
|||||  
Sbjct: 7922 cgcgccacggcgccgtgct 7942

>gi|32567975|gb|AC105258.2| **D** Oryza sativa (japonica cultivar-group) chromosome 5  
complete sequence  
Length = 71145

Score = 42.1 bits (21), Expect = 3.9  
Identities = 21/21 (100%)  
Strand = Plus / Plus

Query: 304 cctccgcggccacggcgccg 324  
|||||||  
Sbjct: 20100 cctccgcggccacggcgccg 20120

>gi|31431814|gb|AE017089.1| **D** Oryza sativa (japonica cultivar-group) chromosome 10  
of the complete sequence  
Length = 300029

Score = 42.1 bits (21), Expect = 3.9  
Identities = 24/25 (96%)  
Strand = Plus / Plus

Query: 749 cttctgcgccgcccagccgcttcttc 773  
||||||| |||||  
Sbjct: 67166 cttctgcgccgtcagccgcttcttc 67190

>gi|24418066|gb|AC009108.10| **D** Homo sapiens chromosome 16 clone RP11-46309, comple  
Length = 168656

Score = 42.1 bits (21), Expect = 3.9  
Identities = 21/21 (100%)  
Strand = Plus / Plus

Query: 719 gcctgccgccgccgcggggcc 739  
|||||||  
Sbjct: 134923 gcctgccgccgccgcggggcc 134943

>gi|44886087|dbj|AB164051.1| Oryzias latipes cGK I beta mRNA for cGMP-dependent pr  
beta, complete cds  
Length = 2506

Score = 42.1 bits (21), Expect = 3.9  
Identities = 21/21 (100%)  
Strand = Plus / Minus

Query: 1198 ccgtcctcatcatgatcgtct 1218  
|||||||  
Sbjct: 891 ccgtcctcatcatgatcgtct 871

>gi|44886085|dbj|AB164050.1| Oryzias latipes cGK I alpha mRNA for cGMP-dependent p  
alpha, complete cds  
Length = 2579

Score = 42.1 bits (21), Expect = 3.9  
Identities = 21/21 (100%)  
Strand = Plus / Minus



Query: 1198 ccgtcctcatcatgatcgtct 1218  
 |||  
 Sbjct: 964 ccgtcctcatcatgatcgtct 944

>gi|29366932|gb|AC009033.10| **D** Homo sapiens chromosome 16 clone RP11-140I24, compl  
 Length = 158628

Score = 42.1 bits (21), Expect = 3.9  
 Identities = 21/21 (100%)  
 Strand = Plus / Minus

Query: 682 ccttcctggacctcttcaactc 702  
 |||  
 Sbjct: 72712 ccttcctggacctcttcaactc 72692

>gi|13424739|gb|AE005972.1| **D** Caulobacter crescentus CB15 section 298 of 359 of th  
 Length = 11923

Score = 42.1 bits (21), Expect = 3.9  
 Identities = 21/21 (100%)  
 Strand = Plus / Plus

Query: 1251 ctggtgctgctggccgccgcc 1271  
 |||  
 Sbjct: 6287 ctggtgctgctggccgccgcc 6307

|        |       |      |
|--------|-------|------|
| Lambda | K     | H    |
| 1.37   | 0.711 | 1.31 |

|        |       |      |
|--------|-------|------|
| Gapped |       |      |
| Lambda | K     | H    |
| 1.37   | 0.711 | 1.31 |

Gap Penalties: Existence: 5, Extension: 2  
 Number of Hits to DB: 14,905,373  
 Number of Sequences: 2102977  
 Number of extensions: 5816  
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 Number of sequences better than 10.0: 0  
 Number of HSP's better than 10.0 without gapping: 0  
 Number of HSP's successfully gapped in prelim test: 18  
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 A: 0  
 X1: 11 (20.0 bits)  
 X2: 15 (30.0 bits)  
 X3: 25 (50.0 bits)

S1: 12 (25.0 bits)



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☐ 1: M76676. Homo sapiens leuk...[gi:2810988]

Links

LOCUS HUMNPIIY20 1481 bp mRNA linear PRI 27-JAN-1998  
DEFINITION Homo sapiens leukocyte platelet-activating factor receptor mRNA,  
complete cds.  
ACCESSION M76676  
VERSION M76676.1 GI:2810988  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1481)  
AUTHORS Kunz, D., Gerard, N.P. and Gerard, C.  
TITLE The human leukocyte platelet-activating factor receptor. cDNA  
cloning, cell surface expression, and construction of a novel  
epitope-bearing analog  
JOURNAL J. Biol. Chem. 267 (13), 9101-9106 (1992)  
MEDLINE 92250505  
PUBMED 1374385  
COMMENT On Jan 27, 1998 this sequence version replaced gi:189269.  
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## ORIGIN

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Mar 11 2004 07:26:05



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1: AY255588. Homo sapiens leuk...[gi:29611577]

LOCUS AY255588 546 bp mRNA linear PRI 08-APR-2003  
DEFINITION Homo sapiens leukocyte platelet-activating factor receptor mRNA,  
partial cds.

ACCESSION AY255588  
VERSION AY255588.1 GI:29611577

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 546)

AUTHORS Vassilatis,D.K., Hohmann,J.G., Zeng,H., Li,F., Ranchalis,J.E.,  
Mortrud,M.T., Brown,A., Rodriguez,S.S., Weller,J.R., Wright,A.C.,  
Bergmann,J.E. and Gaitanaris,G.A.

TITLE The G Protein-Coupled Receptor Repertoires of Human and Mouse

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (8), 4903-4908 (2003)

REFERENCE 2 (bases 1 to 546)

AUTHORS Vassilatis,D.K., Hohmann,J.G., Zeng,H., Li,F., Ranchalis,J.E.,  
Mortrud,M.T., Brown,A., Rodriguez,S.S., Weller,J.R., Wright,A.C.,  
Bergmann,J.E. and Gaitanaris,G.A.

TITLE Direct Submission

JOURNAL Submitted (14-MAR-2003) Primal, Inc., 1124 Columbia Street,  
Seattle, WA 98104, USA

FEATURES Location/Qualifiers

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Links

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 AUTHORS Fredriksson,R., Hoglund,P.J., Gloriam,D.E., Lagerstrom,M.C. and  
 Schioth,H.B.  
 TITLE Seven evolutionarily conserved human rhodopsin G protein-coupled  
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 JOURNAL FEBS Lett. 554 (3), 381-388 (2003)  
 PUBMED [14623098](#)  
 REFERENCE 2 (bases 1 to 1485)  
 AUTHORS Kunz,D., Gerard,N.P. and Gerard,C.  
 TITLE The human leukocyte platelet-activating factor receptor. cDNA  
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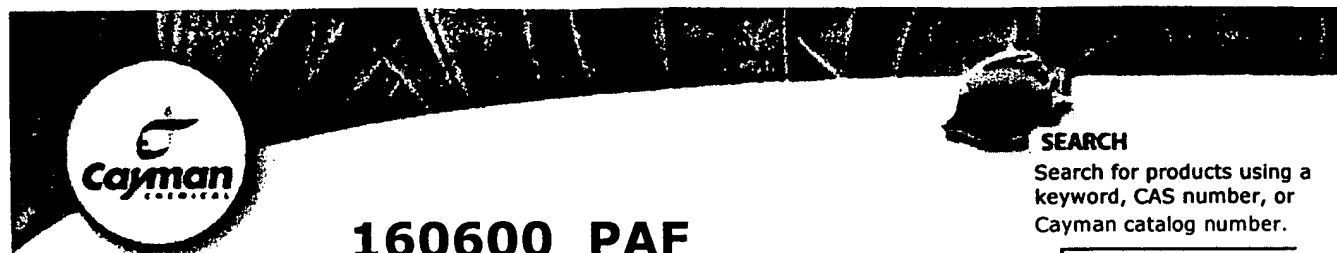


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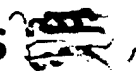
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biological actions by  
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receptor. The PAF  
receptor has been  
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of species including  
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protein coupled receptor. The PAF receptor has been cloned from a number of species including human, rat, and guinea pig and is characterized as a 7-transmembrane receptor which induces phosphoinositol turnover through G-protein coupling.<sup>1 2 3 4</sup> Northern blot analysis reveals that the receptor is expressed in leukocytes, placenta, lung, spleen, small intestine, kidney, liver, and brain.<sup>3 4</sup> In leukocyte cell populations the receptor is found on platelets, myocytes, neutrophils, and B-cells, whereas resting T-cells and natural killer cell lines do not express the PAF receptor.<sup>6</sup> Human monocytes treated with INF- $\gamma$  have a 2-6 fold increase in PAF receptor expression compared to untreated cells.<sup>7</sup>

<sup>1</sup> Nakamura, M., Honda, Z.,

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izumi, I., et al. Molecular cloning and expression of platelet-activating factor receptor from human leukocytes. *J. Biol. Chem.* 266, 20400-20405 (1991).

<sup>2</sup> Kunz, D., Gerard, N.P., and Gerard, C. The human leukocyte platelet-activating factor receptor. cDNA cloning, cell surface expression, and construction of a novel epitope-bearing analog. *J. Biol. Chem.* 267, 9101-9106 (1992).

<sup>3</sup> Ye, R.D., Prossnitz, E.R., Zou, A., et al. Characterization of a human cDNA that encodes a functional receptor for platelet activating factor. *Biochem. Biophys. Res. Commun.* 180, 105-111 (1991).

<sup>4</sup> Bito, H., Honda, Z., Nakamura, M., et al. Cloning, expression and tissue distribution of rat platelet-activating-factor-receptor cDNA. *Eur. J. Biochem.* 227, 211-218 (1994).

<sup>5</sup> Honda, Z., Nakamura, M., Miki, I., et al. Cloning by functional expression of platelet-activating factor receptor from guinea-pig lung. *Nature* 349, 342-346 (1991).

<sup>6</sup> Müller, E., Dagenais, P.,

Alami, N., et al. Identification and functional characterization of platelet-activating factor receptors in human leukocyte populations using polyclonal anti-peptide antibody. Proc. Natl. Acad. Sci. USA 90, 5818-5822 (1993).

<sup>7</sup> Quellet, S., Müller, E., and Rola-Pleszczynski, M. IFN- $\gamma$  up-regulates platelet-activating factor receptor gene expression in human monocytes. J. Immunol. 152, 5092-5099 (1994).

### General References

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| <input type="checkbox"/> | IOH3294  | Human   | complement component 5 receptor 1 (CSa ligand); complement component-5 receptor-2 (CSa ligand)                                                                                                                      | CSR1        |
| <input type="checkbox"/> | IOH12614 | Human   | purinergic receptor P2Y, G-protein coupled, 11                                                                                                                                                                      | P2RY11      |
| <input type="checkbox"/> | IOH22483 | Human   | clone MGC:33224 IMAGE:5267661, mRNA, complete cds.                                                                                                                                                                  | RDC1        |
| <input type="checkbox"/> | IOH14039 | Human   | Similar to putative nuclear protein ORF1-FL49                                                                                                                                                                       | ORF1-FL49   |
| <input type="checkbox"/> | IOH11484 | Human   | glycoprotein Ib (platelet), alpha polypeptide                                                                                                                                                                       | GP1BA       |
| <input type="checkbox"/> | IOH1987  | Human   | tachykinin receptor 1 isoform short; NK-1 receptor; Tachykinin receptor 1 (substance P receptor; neurokinin-1 receptor); tachykinin 1 receptor (substance P receptor; neurokinin 1 receptor); neurokinin 1 receptor | TACR1       |
| <input type="checkbox"/> | IOH13056 | Human   | similar to POSSIBLE GUSTATORY RECEPTOR CLONE PTE01                                                                                                                                                                  | LOC11513    |
| <input type="checkbox"/> | IOH9916  | Human   | coagulation factor II (thrombin) receptor-like 1                                                                                                                                                                    | F2RL1       |
| <input type="checkbox"/> | IOH9624  | Human   | vesicovacuolar intestinal peptide receptor 2                                                                                                                                                                        | VIPR2       |
| <input type="checkbox"/> | IOH10679 | Human   | endothelin receptor type A                                                                                                                                                                                          | EDNR        |
| <input type="checkbox"/> | IOH22637 | Human   | Similar to parathyroid hormone receptor 1, clone MGC34562 IMAGE:516085, mRNA, complete cds.                                                                                                                         | PTH1R       |
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| <input type="checkbox"/> | IOH11033 | Human   | endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4; G protein-coupled receptor; LPA receptor EDG4; Lysophosphatidic acid receptor EDG4                                                | EDG4        |
| <input type="checkbox"/> | IOH10866 | Human   | CD97 antigen isoform 2 precursor; leukocyte antigen CD97; seven-span transmembrane protein                                                                                                                          | CD97        |
| <input type="checkbox"/> | IOH22632 | Human   | formyl peptide receptor-like 1; Spenin A4 receptor (formyl peptide receptor related)                                                                                                                                | FPRL1       |
| <input type="checkbox"/> | IOH22662 | Human   | adrenomedullin receptor                                                                                                                                                                                             | ADM         |
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**R**ecently a novel human G-protein coupled receptor gene has been characterized and mapped to chromosome 2p16. This gene codes for a 540 amino acid protein in retinal pigment epithelium (RPE) and cells surrounding retinal arterioles. In contrast, the Northern blot data obtained from mouse sections suggest the expression of transcripts in photoreceptor inner segments and outer plexiform layer. The transcripts of the GPCR-75 gene (7kb) are also found in abundance in brain sections. So far, no mutations in GPCR-75 protein were identified in patients suffering from Doyme's honeycomb retinal dystrophy (DHRD), an inherited retinal degeneration disease that maps to chromosome 2p16 (1).

The GPCR-75 protein is approximately 78 kDa (540 amino acids) protein that is primarily expressed in human retinal pigment epithelium (RPEs). The GPCR-75 sequence analyses suggest the presence of 7 trans-membrane domains, a characteristic feature of GPCR. The protein has putative N-glycosylation sites near the extra cellular N-terminal end of the proteins. The protein has a large 3 intra cellular loop which might be the site for interaction of G-proteins. The short carboxy terminal is intracellular and has putative post-translational modification lipid modification sites.

The Anti-GPCR-75-selective antibodies were generated against conserved sequences near N- and C-termini of the protein that are unique to GPCR-75 protein. The polyclonal antibody strongly labels a 78 kDa protein in RPE cell extracts. Anti-GPCR-75-selective antibody is also available in affinity-purified form for confocal, Western blotting and immunocytochemical analyses. *FabGennix Int. Inc.* will also conjugate antibodies with fluorescent probes upon request at extra charge. *FabGennix Int. Inc.* will also provides antibodies against proteins that are involved in retinal degenerative diseases such as various Anti-PDE antibodies, Anti-MERTK, Anti-Phospho-MERTK, EGF-containing fibulin like intracellular protein (EFEMP1), Anti-Myocilin (TIGR), Anti-Bestrophin, Anti-ELVOL4 and a Usher syndrome specific Anti-USH2a antibodies etc. *FabGennix Int. Inc.* employs cyclic peptide methodology for generating antibodies, which results in higher titer and specificity (2). *FabGennix Int. Inc.*, will also provide Western blot positive controls for most of these antibodies in ready-to-use buffer for easy identification of respective proteins. Limited quantities of antigens are also available. Please enquire for their availability before ordering.

| Catalog #    | Host Species | Nature                | Cross reactivity | Quantity  | volume  | Price     |
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| GPCR75-100P  | Rabbit       | Polyclonal antisera   | R, M, H          | 100 ml    | 100 ul  | \$ 195.00 |
| GPCR75-101AP | Rabbit       | Affinity purified IgG | R, M, H          | 100 ug    | 150 ul  | \$ 225.00 |
| GPCR75-112AP | Rabbit       | Affinity purified IgG | R, M, H          | 100 ug    | 150 ul  | \$ 225.00 |
| PC-GPCR75    | N/A          | WB positive control   | Rat              | For 5 App | 60 ul   | \$ 75.00  |
| P-GPCR75     | N/A          | Antigenic peptides    | n/a              | 250 ug    | Inquire | \$ 65.00  |

R = rat; M = mouse; H = human; C = chicken; monk = monkey; \* not all variants are labeled equally

**Immunogen:** Synthetic cyclic peptide (GPCR75-101AP = PNATSLHVPHSQEGNSTS-amide; GPCR75-112AP = STSLQBLQLIHTATLVTC-amide).

**Concentration:** GPCR75-101AP, GPCR-112AP IgG concentration 0.75-1.25 mg/ml in 50% antibody stabilization buffer.

**Applications:** Antibody GPCR75-100/GPCR75-101AP are ideal for WB, IEM and EIC assays. The dilutions for this antibody is for reference only, investigators are expected to determine the optimal conditions for specific assay in their laboratory. Dilutions: WB > 1:500; Immunoprecipitation & Lip pull-down assays > 1:250

**Reactivity:** This antibody detects a single 78 kDa Orphan GPCR75 protein in human RPE cell extracts.

**Protocols:** Standard protocol for various applications (WB, IEM and EIC) of this antibody is provided with the product specification sheet, however, *FabGennix Int. Inc.* strongly recommends investigators to optimize conditions for use of this antibody in their laboratories.

**Form/Storage:** The antiserum is supplied in antibody stabilization buffer with 0.02% sodium azide or thimerosal/methionine as preservative. The affinity-purified antibodies are purified on antigen-sepharose affinity column and supplied as 1-1.25 mg/ml IgG in antibody stabilization buffer containing preservatives with low viscosity and cryogenic properties. For long-term storage of antibodies, store at -20°C. Now these antibodies can be stored at -20°C and used immediately with out thawing. *FabGennix Inc.* does not recommend storage of very dilute antibody solutions unless they are prepared in specially formulated multi use antibody dilution buffer (Cat # DiluBuffer). Working solutions of antibodies in DiluBuffer should be filtered through 0.45µm filter after every use for long-term storage.

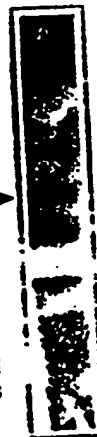
#### References:

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\* For users who may require large amounts of GPCR75-100P or GPCR75-101AP, please enquire about bulk material discounts.  
This Product is for Research Use Only and is NOT intended for use in humans or clinical diagnosis.

061901-0020SF1001Z-REV10.00

78 kDa Orphan Receptor-75  
in human RPE cells.  
Antibody GPCR-100P  
(1:400)



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## Rat Taste Receptor 2 (TR2) Antibodies

Rat Taste Receptor 2 (TR2) Antibodies

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Cat. # TR21-P, Rat TR2 Control Peptide # 1, SIZE: 100 ug/100 ul  
FORM: ☒ Soln ☒ Lyophilized Lot # 3113P

Cat. # TR21-S, Rabbit Anti-rat TR2 antiserum # 1, SIZE: 100 ul neat antiserum  
FORM: ☒ Soln ☒ Lyophilized. Lot # 38889S

Cat. # TR21-A, Rabbit Anti-rat TR2 Ab # 1 (affinity pure) SIZE: 100 ug  
FORM: ☒ Soln ☒ Lyophilized. Lot # 38889A

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Higher vertebrates are believed to possess at least five basic tastes: Sweet, bitter, sour, salty, and unami (the taste of monosodium glutamate). Taste receptor cells that may selectively reside in various parts of the tongue and respond to different tastants and perceive these taste modalities. Circumvallate papillae, found at the very back of the tongue, are particularly sensitive to bitter substances. Foliate papillae, found at the posterior lateral edge of the tongue, are sensitive to sour and bitter. Fungiform papillae at the front of the tongue specialize in sweet taste.

Recently, two novel taste receptors, TR1 and TR2, have been cloned with distinct topographical distribution in taste receptor cells and taste buds. TRs are members of a new group of 7 TM domain containing GPCR distantly related to other chemosensory receptors (Ca<sup>2+</sup>-sensing receptor (CaSR, a family of putative hormone receptor (V2R), and metabotropic glutamate receptors). TR1 is expressed in all fungiform taste buds, whereas TR2 localized to the circumvallate taste buds. Both receptors do not co-localize with gustducin.

### Source of Antigen and Antibodies

TR1 (rat 840 aa) and TR2 (rat 843 aa) share ~40% homology with each other, and ~30% with CaSR, and 22-30% with V2R pheromone receptors and mGLURs. Rat TR are 7 TM domain containing protein with an extra long N-terminal, extracellular domain (1). A 19 AA Peptide (designated TR21-P; control peptide) sequence near the C-terminus of rat TR2(1) was selected for antibody production. The peptide was coupled to KLH, and antibodies generated in rabbits. Antibody has been affinity purified using control peptide-Sepharose.

### Form & Storage

Control peptide Solution is provided in PBS, pH 7.4 at 1 mg/ml (100 ug/100 ul). Antiserum is supplied as neat serum (100 ul soln or lyophilized). Affinity pure antibodies were purified over the peptide-Sepharose column and supplied as 1 mg/ml soln in PBS, pH 7.4 and 0.1% BSA as stabilizer (100 ul in solution or Lyophilized).

The peptides and antibodies also contain 0.1% sodium azide as preservative. Lyophilized products should be reconstituted in 100 ul water and gently mixed for 15 min at room temp. All peptide/antibody

received in solution or

reconstituted from lyophilized vials should be stored frozen at -20°C or below in suitable aliquots. It is not recommended to store diluted solutions. Avoid repeated freeze and thaw.

#### Recommended Usage

Western Blotting (1:1K-5K for neat serum and 1-10 ug/ml for affinity pure antibody using ECL technique).

ELISA: Control peptide can be used to coat ELISA plates at 1 ug/ml and detected with antibodies (1:10-50K for neat serum and 0.5-1 ug/ml for affinity pure).

**Histochemistry & Immunofluorescence:** We recommend the use of affinity purified antibody at 1-20 ug/ml in paraformaldehyde fixed sections of tissues (1).

#### Specificity & Cross-reactivity

The 19 AA rat TR21-P control peptide is specific for rat TR2. It has no significant sequence homology with TR1 or gustducin or pheromone receptors. Antibody cross-reactivity in various species has not been studied. The TR21-P control peptide is available to confirm specificity of antibodies.

#### References:

1. Hoon MA et al (1999) Cell 96, 541-555; Lindemann B (1999) Nature Med. 5, 381-382

"Neat Antisera" are the unpurified antiserum and it is suitable for ELISA and Western.

"Affinity pure" antibodies have been over the antigen-affinity column and recommended for immunohistochemical applications.

"Control peptides" can not be used for Western as they are very short peptides. They are intended for ELISA or antibody competition studies.

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